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July 29, 2003, 13:42:08; Search time 99 Seconds (Without alignments) 1099.982 Million cell updates/sec
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1 MQQPQPQGQQQPGPGQQLGG......KSLVQIHEKNGWYTPPKEDG 422
                                                                                                                                                                                                                                                                                                                                                                    830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                       Title:
Perfect score:
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1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mannal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_plant:\*
10: sp\_plant:\*
11: sp\_rodent:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_unclassified:\*
15: sp\_virus:\*
16: sp\_arvirus:\*
17: sp\_archeap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	228 O8k2z8 mis misculu		C	1 09d7e1 mis		One abridge	C	מ			0			7:00.00 7:00.00	#nc100	80[06D		שניינוסיי
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dР	Query	65.0	64.8	64.4	58.7	53.4	51.6	50.1	50.1	49.7		45.8	43.3	37.7	36.2	32 7		77.00	16.3
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17         343         15.4         71         4         08N4G6           18         140         6.3         425         5         095039           20         136.5         6.1         189         5         09R8K6           21         136.5         6.1         199         5         09R8K6           22         133         6.0         1300         12         036421           23         131.5         5.9         424         4         08W8K6           24         131.5         5.9         424         4         08W8K4           25         131.5         5.9         501         4         08WWB4           25         131.5         5.9         523         4         09933           27         128         5.7         4         08WWB4           28         127.5         5.7         4         09933           29         127.5         5.7         4         09937           30         127.5         5.7         20         1         09146           31         127.5         5.7         20         1         09146           32         127.5 <t< th=""><th>Q8n4g6 homo sapien Q95039 paramecium Q8n8k6 homo sapien Q81026 bombyx mori P91633 drosophila</th><th></th><th>000301 homo sapien 0969t4 homo sapien 091x63 mus musculu 09uqh5 homo sapien 061580 drosophila 08151y1 mus musculu</th><th>Q9h6u9 homo sapien Q9h016 rattus norv Q92603 homo sapien Q00211 homo sapien Q9h2q2 homo sapien Q8haq2 homo sapien</th><th></th></t<>	Q8n4g6 homo sapien Q95039 paramecium Q8n8k6 homo sapien Q81026 bombyx mori P91633 drosophila		000301 homo sapien 0969t4 homo sapien 091x63 mus musculu 09uqh5 homo sapien 061580 drosophila 08151y1 mus musculu	Q9h6u9 homo sapien Q9h016 rattus norv Q92603 homo sapien Q00211 homo sapien Q9h2q2 homo sapien Q8haq2 homo sapien	
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343 15.4 140 6.3 136.5 138 6.2 138 6.0 131 5 6.1 131 5 6.1 121 5 5.9 121 5 5.9 127 5 5.7 127 5 7.7 127 5 7.7 127 5 7.7 127 5 7.7 128 5 7.7 127 5 7.7 128 5 7.7 127 5 7.7 128 5 8 8 8 7.7 128 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	42422	44421			~~
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## ALL GRAMENT

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                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
51milar to NICE-5 protein (EC 6.3.2.19) (Ubiquitin-conjugating enzyme-E2) (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 1448.5; DB 11; Length 378; 74.0%; Pred. No. 1.7e-96; tive 33; Mismatches 52; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . conjugation pathway.
378 AA; 42923 MW; D1690A9C4BC6DBDC CRC64;
                                            3.78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00212; UBCc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 285; Conserv
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                        Q8K2Z8
Q8K2Z8;
RESULT 1
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66

41 LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSV-PG

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SEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS (BY SIMILARITY).

C. -! CATALYIC ACTIVITY: ATP + UBIOUITIN + PROTEIN LYSINE - AMP +
DIPHOSPHATE + PROTEIN N-UBIQUITILISINE.

-! PATHAXY: UBIQUITIN CONJUGATION; SECOND STEP.

-! PATHAXY: UBIQUITIN CONJUGATION; SECOND STEP.

-! HICLESTER FORMATION (BY SIMILARITY).

C. -! MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THOLESTER FORMATION (BY SIMILARITY).

C. -! SIMILARITY: BELLONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

REMBL; BCO17708; AAH17708.1, -.
RINTERPO; IFROUGO68; UBQ_conjugat.

REMBL; BCO17708; UBQ_conjugat; 1.
REMBL; SMO0591; RWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 YNLPKHLDVEMIDQPLPTGQNGTTEEVTSEEEEEEMAEDIEDLDHYEMKEEEPISGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVS
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to NICE-5 protein (EC 6.3.2.19) (Obiquitin-conjugating enzyme
E2) (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAAPGPH-LPPRGSVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNLPQHPDVEMLDQPLPAEQ-CTQEDVSS--EDEDEEMPEDTEDLDHYEMKEEEPAEGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 375;
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSS0127; UBLOUITIN_CONJUGAT_2; 1.
Jbl conjugation pathway.
375 AA; 42818 MW; 7DE07315E89178A3 CRC64;
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                                                                                                                  422
                                                                                                                               PRT;
                                                                                                                  AQQSYKSLVQIHERNGWYTPPKEDG
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00212; UBCc;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
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Ligase; Ubl c
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                                                     DPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKL 159
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                                                                                                                                                                                                                                                                    --PPPPPPGSSLSPP
                                                                        EDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVE
                                                                                                                                                                                                                                                  LVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSP
                                                                                                                    YNLPQHPDVEMLDQPLPAEQ--CTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Wature 420:563-573(2002).

EMBL; AKOB3216; BAC38013.1; -. SEQUENCE 378 AA; 42950 MW; 4A81CA85400A1313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.8%; Score 1445.5; DB 11; Length 378; 73.8%; Pred. No. 2.8e-96; tive 34; Mismatches 52; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to NICE-5 protein homolog.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
        AQOSYNSIVQIHEKNGWYTPPKEDG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-Hippocampus; MEDLINE-22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8BUN2;
01-MAR-2003
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                        PVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

A Marai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Sogabe Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Tongue;
MEDILIFE-22354681; PubMed-12466851;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carning P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Norazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310012MH3 product:NICE-5 FROTEIN (PRO3094) homolog.
Mus musculus (Mouse)
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musine; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                    253 AA.
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                                                                                                                         RAQQSYKSLVQIHEKNGWYTPPKEDG
                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=20499374; Pubmed=11042159;
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Tongue;
MEDILINE-99279233; Pubmed-10349636;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=20530913; PubMed=11076861;
                                                                                                                                                                                                                                                                  PRELIMINARY;
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Q9D7E1;
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

LO CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).

- I- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE - AMP +

DIPHOSPHATE + PROTEIN N-UBIQUITIN/SINE).

- I- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.

- I- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.

- I- MISCELLANEOGS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-

THIOLESTER FORMATION (BY SIMILARITY).

- INILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

EMBL; BC000848; AAH00848:1; -

INILARITY: BLONGS (B) UB_Conjugat.

R PFODOM; PD000461; UBQ_Conjugat.

R PRODOM; PD000129; UBCC; 1.

R PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

R PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

M Hypothetical protein; Ligase; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 ICMELLTKOGWSSAYSIESVIMOISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIH 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 LEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Aliyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakayuchi S., Ikegami T., Kashiyagi K., Yoneda Y., Ishikawa T., Ogawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequence."; EMBL. AC009324; BABIZ6217.2; SEQUENCE 253 AA; 28487 MW; BFB9519FF26585CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 253;
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
HypothetLcal ubjquitin-protein 11gase (EC 6.3.2.19)
conjugating enzyme E2) (Ubjquitin carrier protein)
                                                                                                                                                                                                                                                                                                                                                                                                       58.7%; Score 1308; DB 11;
99.6%; Pred. No. 1.4e-86;
rative 1; Mismatches 0;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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us-10-005-549-2.rspt

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A Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Ratanabe M., Fulimori K., Tanai H., Tahida M., Yamashita H., Chiba Y.,
A Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
A Watanabe M., Fulimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
A Watanabe M., Fulimori K., Tanai H., Saito K., Nishikawa T.,
A Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
A Kimura K., Matsuo K., Nakamura Y., Saito K., Nishikawa T.,
A Kimura K., Matsuo K., Nakamura Y., Saito K., Nishikawa T.,
A Wagatsuma M., Takahashi-Fujii A., Sohima M., Kawakami B.,
A Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
A NEDO human cDNA sequencing project.";
A NEDO human cDNA sequencing project.";
B NEDO human cDNA sequencing project.";
C -- FUNCTION: CRIALIZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
PROTEINS (BY SIMILARITY).
C -- CATALIZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
C -- PATHWAY: UBIQUITIN N-UBIQUITIN. PROTEIN LYSINE - AMP +
DIPHOSPHATE + PROTEIN N-UBIQUITIN. SECOND STEP.
C -- PATHWAY: OBIQUITIN RESIDINE IS REQUIRED FOR UBIQUITIN-
C -- MISCELLANEOUS A CYSTENDE RESIDINE IS REQUIRED FOR UBIQUITIN-
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EMBL; AKO56388; BAB71173.1; -.
                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FL31826 (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin-protein ligase) (Ubiquitin carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostom1;
HOMO.
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PROSTIE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Hypothetical protein; Ligase; Ubl conjugation pathway.
SEQUENCE 217 AA; 24277 MW; 3C74AF937AE2BCCE CRC64;
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae,
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                                                                            349 RVYKSMVLKHEKSGWFTPPQKDG
                                                   400 QSYKSLVQIHERNGWYTPPKEDG
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Best Local Similarity 100.0
Matches 217; Conservative
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                                                                                                                                                                                                                                            253 TDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGA 312
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                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-Ovary;
MEDLINE-223546893; PubMed=12466851;
The FANTOM CONSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLPQHPDVEMLDQPLP-AEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELV
                                                                                                                                                                                                                                                                                                                                          DFILLINFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMO
                                                                                                                                                                                                                                                                                                                                                                EMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQA
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 1149.5; DB 11; Length 371; 60.3%; Pred. No. 6.5e-75; ive 61; Mismatches 74; Indels 17;
                                                                                                    ô
                                                      Length 230;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK054382; BAC35757.1; -.
SEQUENCE 371 AA; 42237 MW; BPODA7D1B3045C05 CRC64;
    97C13304B8E1D6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                  0;
                                                   Score 1191; DB 4;
Pred. No. 3.3e-78;
                                  53.4%; Scc. 100.0%; Pred. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequ
01-WAR-2003 (TrEMBLrel. 23, Last anno
Similar to similar to NICE-5 protein.
       25882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                Conservative
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       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231;
                                                                                                Matches 230;
                                                                                                                                              193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
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                                                                                                                                                                                                                                                                                                                                                                                                                                     373
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       SEQUENCE
                                                 Query Match
                                                                                                                                                                                                                                                                                        61
                                                                              Local
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Matches
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Q8BW45
       g
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Gaps

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120

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the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based or 60,770 full-length cDNAs.";
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                                                                                   49.78;
                                                                                                                                                                                                                                                                                                                          408 IHEKNGWYTPPKEDG 422
                                                                                                                                                                                                                                                                                                                                      241 IHEKNGWYTPPKEDG 255
                                                                                               Best_Local Similarity 83.19
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQ 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last anotation update)
01-MAR-2003 (TrEMBLrel. 23, Last anotation update)
similar to EG:25E8.2 gene product (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin-protein ligase) (Ubiquitin carrier
                                                                                                                                                                          Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 MKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; BC030044; AAH30044.1; -.
MGD; MGI:1917343; 2310012M18Rik.
InterPro; IPR000608; UBQ_conjugat.
                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                  DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
-I-PATHARY: UBIQUITIN CONJUGATION; SECOND STEP.
-I-MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
                                                                                                                                                                                                           PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                              50.1%; Score 1117; DB 11; Length 217; llarity 100.0%; Pred. No. 6.8e-73; Conservative 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                              conjugation pathway.
217 AA; 24277 MW; 3C74AF937AE2BCCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGANKSQYSLTRAQQSYKSLVQIHEKNGWYTPPKEDG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AA.
                                                                                                                                                                                                                                                                                                                           Pram; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
SMART; SM00212; UBCc; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/63; TISSUE-Head;
MEDLINE-22354683; PubMed-12466851;
The FANTOM CONSOITIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                               TISSUE-Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                             NCBI_TaxID-10090;
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                                                                           2310012M18RIK.
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SEQUENCE 2
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                                                                     protein)
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RKA MEDEINELEST, WALAN-BERKELEKY, RAIN-BERKELEKY, RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Cabburner M., Henderson S.N., Stuton G.G., Wortman J.R., Yadadal M.D., Zhang O., Chen L.X., Rander R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Boslakov S., Borkova D., Botchan M.P., Butler H., Cadieu E., Center A., Chandra I., RA Beeson K.Y., Benos P.V., Butler H., Cadieu E., Center A., Chandra I., Ra Ballos B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews A., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Andrews M., Duckon K.J., Evangelista C.C., Ferriara C., Ferriara C., Gabriellan A., Galas R., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Xetchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Xetchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Liang Y., Lin X., Liang Y., Liu X., Liang Y., Liu X., Liang Y., Liu X., Liang Y., Liang Y., Liang Y., Liang Y., Liang
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p Phase I & II Team;
on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 MLDQPLPAEQ--CTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AILEKIKKNORODYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 VKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGG
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     7,
                                                                                                                                                                                                                                                                                                        49.7%; Score 1107; DB 11; Length 255; 83.1%; Pred. No. 4.5e-72; ive 20; Mismatches 21; Indels 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olymar-2000 (TrEMBLrel. 13, Created)
Ol-Mar-2000 (TrEMBLrel. 13, Last sequence update)
Ol-OCT-2000 (TrEMBLrel. 22, Last sequence update)
Ol-OCT-2002 (TrEMBLrel. 22, Last annotation update)
EG:155B.2 protein (EC 6.3.2.19).
EG:25EB.2 protein (EC 6.3.2.19).
EG:25EB.2 protein (Eruit fly).
ENOSOPHIA melanogaster (Fruit fly).
ENdaryota: Metazoa: Arthropoda: Hexapoda: Insecta; Pterygoi Neoptera: Endopterygota: Diptera: Brachycera; Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.
                                                                          60,770 full-length cDNas.";
Nature 420:563-573(2002).
EMBL; AK076148; BAC36218.1; -.
SEQUENCE 255 Aa; 28916 MW; 2F5077B3FAC2D6DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
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394

PRT;

PRELIMINARY;

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., My M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Relson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spler E., Stradling A.C., Stapheton M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Spler E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yang Z.-Y., Rassaman D.A., Weinstey K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong W., Rubin G.M., Venter J.C.;
RA Zheng X.H., Anyers E.W., Rubin G.W., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
C. -- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
C. -- PROFEINS (BY SUMILARITY).
C. -- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE - AMP +
DIPHOSPHAFE + PROTEIN N-UBIQUITYLLSINE.
C. -- PATHRAY UBIQUITIN CONJUGATION; SECOND STEP.
THIOLESTER FORMATION (BY SILMLARITY BELLONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
BEMBI, AEDO3423; AAR457671; --
C. -- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
BEMBI, AEDO3423; AAR457681; --
C. -- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
BEMBI, AEDO3423; AAR457681; --
C. -- SIMILARITY: BELONGOB; HOL.CONJUGATING ENZYME FAMILY.
BEMBI, AEDO3423; AAR457681; --
BENERAL PERONGOB; HOL.CONJUGATION CONJUGATING ENZYME FAMILY.
BEMBI, AEDO3423; AAR457681; --
BENERAL PERONGOB; HOL.CONJUGATING ENZYME FAMILY.
BENERAL PERONGOB; HOL.CONJUGATING ENZYME FAMILY.
BENERAL PERONGOB; HOLCONJUGATING ENZYME F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 KEEEPAEGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 RIMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 ILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 ATLVKGKARVQFGANKS----QYSLTRAQQSYKSLVQIHEKNGWYTPPKEDG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.8%; Score 1020.5; DB 5; Length 397; llarity 49.0%; Pred. No. 1.5e-65; Conservative 72; Mismatches 87; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 MISSING (IN SHORT ISOFORM)
44391 MW; 37081F41680C9D9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50127; UBIQUITIN_CONJUGAR_2; 1.
Hypothetical protein; Alternative splicing; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conjugation pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AA;
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Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 RYDIHANITETYPSSPPVWFAESEETSVTNAVQILSNTNGRDNHVINQVGILLRELCRLH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 NLPQHPDVEMLDQPLPAEQCTQEDVSSEDE------DEEMPEDTEDLDHYEM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 NVPLPPDIDNLALPLOTPPPSASPLRCEQRPGGGGAGGGGGPHGNEETDSDQEEIEDPIG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEEEPAEGKK------SEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 ESEQESEGDEDLPLEMDDVRSTSKKDDMEVEHLATLEKLRQSQRQDYLKGSVSGSVQATD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 RIMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 ILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- DKNGK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 PVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEINS CATIVITY: ATP + UBIOUTIN OF OBJUILLIN OF OF PROTEINS OF STRUKTERING.

-! CATALYTIC ACTIVITY: ATP + UBIOUTIN + PROTEIN LYSINE - AMP + DIPHOSPHATE + PROTEIN N-UBIOUTINLESINE.
-! PATHAAX: UBIOUTIN CONJUGATION; SECOND STEP.
-! MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; ALO09196; CAA15712.1; -
-! SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; ALO09196; CAA15712.1; -
-! FIDHOUGAS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
FEMBL; ALOO9196; UBO_CONJUGAT.

PÉRM: PFOOLTS, UD.CON, 1.
                                                                                                                                                                  enzyme E2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Murphy L., Harris D., Barrell B.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
EG:25E8.2 protein (EC 6.3.2.19) (Ubiquitin-conjugating (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . conjugation pathway.
394 AA; 44000 MW; 83E2AFB825D6CD76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATLVKGKARVQFGANKS - - - - QYSLTRAQQSYKSLVQIHEKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.3%; Score 965.5; DB 5
48.1%; Pred. No. 1.4e-61;
ative 71; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ligase; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
                                                                 Created)
                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                 EG:25E8.2 OR CG2924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-7227;
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Best Local Simil
Matches 194; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
SOW REAL PROPERTY OF THE PROPE
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RESULT 12

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCKLYNL------PQHPDV-----EMIDQPLPAEQCTQEDVSSEDEDEEMP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDTE-DLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLMKELRDIYRSQSFKGGNYAVEL-VNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGAD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 ----- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
-i- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 CLRR---ELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 LCSFYNLOMPCELPQIAPPVRDDIDEGRGSDISDITSEPIDDDMAGDGEVDDDDEEEEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS (BY SIMILARITY).
-!-CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
-! PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.
-!- MISCELLANBOUG: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-THOLESTER FORMATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                   enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 100; Indels
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update).
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
F25H2.8 protein (EC 6.3.2.19) (Ubiquitin-conjugating en.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00018; EF HAND; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ligase; Ubl conjugation pathway.
SEQUENCE 471 Aa; 54029 MW; 69EEBCAA5B510D78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 SATLVKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 841; DB 5;
44.9%; Pred. No. 1.7e-52;
iive 69; Mismatches 100
  471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 279754; CAB02096.1; --
WormPep; F25H2.8; CE09653.
InterPro: IPR002048; EF-hand.
InterPro: IPR0020608; UBQ_conjugat.
Pfam; PF00179; UQ_con; I
                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 180; Conservative
PRELIMINARY;
                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00212; UBCc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961
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A PART OF THE PROPERTY OF THE PROPERTY OF THE PARTY OF TH
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217 SEDDGIGKENLAILEKIKKNORODYLNGAVSGSVQATDRIMKELRDIYRSQSFKGGNYAV 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: APP + UBIQUITYLLYSINE.
-!- PATHWAY: UBIQUITYLLYSINE.
-!- PATHWAY: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
-!- THIOLESTER FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 ELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPFVRVVS
                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
GM13209p (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin-EG:25E8.2 OR CG2924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY. EMBL; AY089520; AAL90258.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guarain H., Kronmiller B., Li P., Li Po., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMU0212; UBCC; 1.
PROSITE; PS50127; UBLQUIIN_CONJUGAT_2; 1.
Liqase; UDl conjugation pathway.
SEQUENCE 217 AA; 24605 MW; F42EF12FBDD44AA7 CRC64;
Created)
Last sequence update)
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72.4%; Pred. No. 1.4e-50;
tive 31; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0023528; EG:25E8.2.
InterPro; IPR000608; UBQ_conjugat.
Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patel S., Pl
Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 152;
                          338
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Q96J08;
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O8T3U4;
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Query Match
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                                                                                                                                                                                                                                                                                                                                      DVEMLDQPLPAEQ-CTQEDVSS--EDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIG 223
                                                                                                                                                                                                                                                                                                                                                                          224 KENLAILEKIKKNQRQDYLNGAVSGSVQATDRIMKELRDIYRSQSFKGGNYAVELVNDSL 283
                                                                                                                                                                                                                                                                                                                                                                                                                 YDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGY 343
                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                 2 DVEMLDQPLPTGQNGTTEEVTSEEEEEERARDIEDLDHYEMKEEEPISGKKSEDEGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG4502 protein (EC 6.3.2.19) (LD39243P) (Ubiquitin-conjugating enzyme E2) (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                      MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical ubiquitin-protein ligase (EC 6.3.2.19) (Ubiquitin-
conjugating enzyme E2) (Ubiquitin carrier protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                DB 4; Length 199;
                                                                                                                                                                                                                                                                                                                    26; Indels
                                                                                                                                                                                                                                                                           SEQUENCE 199 AA; 22836 MW; 0523FA017EBE8820 CRC64;
                                                                                                                                                                                                                           Pfam, Pr00179; UQ_con; 1.
Probom; PD000461; UBC_conjugat; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Hypothetical protein; Ligase; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                               Query Match 32.7%; Score 728.5; DB 4 Best Local Similarity 76.2%; Pred. No. 6.8e-45; Mátches 147; Conservative 17; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 VLGGGAICMELLT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 VHPSKGRWLNMLT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                       SEQUENCE FROM N.A.
                                                                                                 TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                    NCBI_TaxID=9606;
                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                 Query Match
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfediffer B.D.,

RA ADII J.F., Apbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baeasley E.M.,

Ballew R.M., Basu A., Barana B.P., Bhandari D., Bolshakov S.,

Banckova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,

Borkova D., Botchan M.R., Buller H., Cadlew E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dalkke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dalkke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dankke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Davens M., Dugan-Rocha S., Plactschman W.,

RA bodson K., Doup L.E., Downes M., Jugan-Rocha S., Plactschman W.,

RA Clodek A., Gong E., Garrell J.H., Gu Z., Gelbart W., Glasser K.,

Alaris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Jalail M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalail M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalail M., Kalush F., Mortlosh T.C., Morteod M.P., Morbherson D.,

K., Mattel B., Morntosh T.C., Morceod M.P., Morbherson D.,

RA, Lasko P., Leil T., Levittsky A.A., Li J., Li Z., Llang Y., Lin X.,

Luu X., Mattel B., Morntosh T.C., Morred M.P., Morbherson D.,

RA, Nelson D.R., Nelson K.A., Juston K., Musskern D.R., Pacleb J.M.,

Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA, Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

Rajazolo M., Hossarman D.A., Reinstock G.M., Weissenbach J.,

RA, Wenger E., Spradling A.C., Stapleton M., Strong R.,

Rang Z.-Y., Wassarman D.A., Reinstock G.M., Weissenbach J.,

Radener R., Rein R.-F., Zaveri J.S., Zhan M., Zhan S., Zhu X., Smith H.O.,

Ry Cheng X.H., Zhong W., Zhong W., Zhun S., Zhu X., Smith H.O.,

The genome sequence of Drosophila melan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 VNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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-!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY EMBL; AE003616; AAR55492.1; --
EMBL; AZ060422; AAL55461.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligase; Ubl conjugation pathway.
SEQUENCE 306 AA; 33669 MW; 75897876D46A813A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.8%; Score 440.5; DB 5; 45.2%; Pred. No. 7.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches
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Search completed: July 29, 2003, 13:47:10 Job time: 102 secs

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August 4, 2003, 14:10:51; Search time 10661 Seconds (without alignments) 8649.310 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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RESULT 1

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BOUNTION Homo sapiens ubiquitin-conjugating enzyme E20 (UBE2Q) mRNA, COMPLET Cds.
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SOURCE
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CORGANISM
HOMO sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3230 bp
MAMMAN E., Schulzee, E., Adham, I., Koehler, M. and Engel, W.
TITLE Isolation and characterization of the human UBE2Q gene and its

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Altmann,M.E.
Direct Submission
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100.0%; Pred. No. 4e.
ive 0; Mismatches
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1. .1330
/organism="Homo sapiens"
/AD_LYPe="genomic DNA"
/AD_LYPe="faxon:9606"
394 a 304 c 303 g 329
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                                                                                                                      Conservative
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OUGLY MATCH 59.0%; Score 1330; DB 6; Length 1330; Best Local Similarity 100.0%; Pred. No. 4e-155; Matches 1330; Conservative 0; Mismatches 0; Indels 0; Gaps 909 CTTGGAGAGGCTGGTGACATAAAGAAAGGGAATACTCTGCTATTGCAGCATCTGAAGAG 9	969 GATCATCTCCGACCTGTGTAAACTCTATAACCTCCTCAGCATCCAGATGTGGAGATGCT 102	109   100	OY 1269 GGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGTTTCAAAGG 1328	1449 AGCCACTTCACTTACTTTCCTTTAACATTACCTTTCCCTTTCCCCACCA	QY         1629         GCAGATCAGTGCCACACTGGTGAAGGGAAAGCACGAGTGCAGTTGGAGCCAACAAATC         1688           P         721         GCAGATCAGTGCCACACTGGTGAAGGGAAAGCACGAGTGCAGTTTGGAGCCAACAAAATC         780           QY         1689         TCAATACAGTCTGACAAGAGCACAGGAGTCCTACAAGTCCTTGGTGCAGATCCACGAAAA         1748           Db         781         TCAATACAGTCTGACAAGAGCACAGGAGTCCTACAAGTCCTTGGTGCAGATCCACGAAAA         840           QY         1749         AAACGGCTGGTACACACACACACAGGCTAACAAGGAGCTTACAAGTCCTTGGTGCAGATCCACCTTCCTCC         1808           PIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1809 CTCCCCAGGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCACGCTGCCT 1868
CTCCCCAGGCACCATTACCTTGAATGCTGTATTGGATCTCACGCTGCT 18	1021 1989 1081 2049 1141	TACCTAIGCATGATTTTAATTTATTTCCTATTCACGACGACGACGACGACGACGACGACGACGACGACGACG	Page 1321   TGTTAATTG 1330   RESULT 6   BD137243   BD	ORGANISM Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 1330)  AUTHORS Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and  TITLE Human nucleic acid sequence originating in prostatic tissue  MCDOSONIAL PACENGE GESELISCHAFT FUER GENOM FORSCHUNG MBH  OS Homo sapiens (human)  PN JP 2002505878-A/4  PD 26-FEB-2002  PD 26-FEB-2002  PD 26-FEB-2002	PR 10-MAR-1998 DE 12000174.2  PR 10-MAR-1998 DE 198 11 134.0  PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY, PI EDGAR DAHL,  PI ANDRE ROSENHHAL  PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P13/08, PC A61P35/00, PC C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, C12N15/02, PC C12P21/02, PC C12P21/03, C12N15/00, A61K37/02, C12N5/00, C12N15/00 CC Human nucleic acid sequence originating in prostatic tissue FH Key CONTICL ACID ANDREA CONTICL ACID ANDREA CONTICL ACID ANDREA CONTICL ACID ANDREA CONTICL ACID ACID ANDREA CONTICL ACID ACID ACID ACID ACID ACID ACID ACID	cation/Qualif .1330 rganism="Homo ol_type="geno b_xref="taxon 304 c 30

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/product="Unknown (protein for IMAGE:3458173)"
/protein_id="AAH00848.1"
/db_xref="G1:12654077"
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ELLTKOGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIN-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabb.remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 4 Row: 1 Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6688150.
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1162)
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          TGGCTATTCTAAACGCTAAGGAAAAAAAAACAAACACAGAACTGTTTCAAGTACTCAAGAC
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                                                                                         GAAACTTTCGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACTAGAGCCTCC
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HOWO Sapiens, clone IMAGE:3458173, mRNA, partial cds.
BC000848
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QY         1932         CTATTCTAAACGCTAAGGAAAAAAACAAACACAGAACTGTTTCAAGTACTCCAAGACTGA         1991           LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         2112 CCTATGCTATGGATTTTTAATTTTCTCTTATTTCATGTACACTGCTTTTTTGGTT 2171           Db         1021 CCTATGCTATGGATTTTTAATTTTTCTCTTATTTCATGTACACTGCTTTTTTTGGTT 1080           QY         2172 ACAGTGTATGATGGATGTGTATGAAAAAATGTATCTTTGGGAAACAATTACAGTTTGT 2231           Db         1081 ACAGTGTATGATGGATGTATGAAAAAAAATGTATCTTTGGGAAACAATTACAGTTTGT 2231           Db         1081 ACAGTGTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		ORGANISM Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Masuho, V.	TITLE Full-length cDNAs  JOURNAL Patent: EP 1293569-A 883 19-MAR-2003;  Helix Research Institute (JP); Research Association for Biotechnology (JP); Research Association for Location/Qualiflers 1. 2523   /organism="Homo sapiens" / /organism="Homo sapiens" / //organism="genomic DNA" / // // // // // // // // // // // //	Query Match         49.5%;         Score 1115.4;         DB 6;         Length 2523;           Best Local Similarity         99.9%;         Pred. No. 1.12-128;         0         Gaps         0;           Matches 1116;         Conservative         0;         Mismatches         1;         Indels         0;           Oy         1126         TATGAAATGAAAGAGCAAGAGCAGCTGAGGCAAGAAATCTGAAGATGATGGCATTGGA         1185           Db         1         TATGAAATGAAAGAGCAAGCAGCTGAGGGAAAAATCTGAAGATGATGGCATTGGA         60	0y         1186 AAAGAAAACTTGGCCATCCTAGAGAAATTAAAAAGAACCAGAGGCAAGATTACTTAAAT 1245           1

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Mus musculus, RIKEN CDNA 2310012M18 gene, clone IMAGE:1054347, BC030344
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1173)
Strausberg,R.
Direct Submission
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                                                                                                                              AACTTTCCCTTTGACCCACCATTTGTCAGGGTTGTGTCTCCAGGCTCTCTGGAGGGTAT
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/note="unnamed protein product"
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/potoein_id="BAB71173.1"
/db_xref="G1:16551781"
/db_xref="G1
                                                                                                                                                                                                                                                                                                                                                                                         Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Blotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan KRy Technology Center etc.); 5'- & 3'-end one pass sequencing: RRy Technology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB, Evaluation; clone selection for full insert sequencing: RAB and
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                                             Ono,Y., Hotuta,T., HIraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Wakanatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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/cell_type="teratocarcinoma"
/clone_lib="NT2RE6"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 5-weeks retinoic acid (RA) induction."
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
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                         Ishibashi, T., Kanehori, K., Yosida, M.,

    .2523
    Organism-"Homo sapiens"
/AD_Lype-"mRNA"
    /Ab_Xref-"taxon:9606"
    /Clone-"NT2RP6000086"

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Homo sapiens, NICE-5 protein, clone MGC:14087 IMAGE:3927447, mRNA,
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
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     CAAAGTTGACCAGGATAGCGCTTTGCACAATGATCTTCAGATCCTGAAGGAGGAAGG
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                                        AGCCGACTTCATCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGACCCCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="Eempedfedledhyemkeeepaeckkseddgigkenlailekikk
NQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKV
DQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAIC
MELLTRQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIH
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Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                         Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of I
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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Pred. No. 4.3e-114;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1054347"
/tlssue_type="Mammary gland"
/clone_lib="Soares_mammary_gland_NbbWG"
/lab_host="DH10B"
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/protein_id="AAH30044.2"
/db_xref="G1:28175091"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="LocusID:70093"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Identification of human epidermal differentiation complex (EDC)-encoded genes by subtractive hybridization of entire YACs a gridded keratinocyte cDNA library Genome Res. 11 (3), 341-355 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 - TCATTTTCCTGGACGTGATAGCTCTGCCTATTGCAGGACAATGATGGTATTCTAAACG
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                                                        Catarrhini; Hominidae;
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Mammalia; Euthería; Primates;
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NICE-5 gene; NICE-5 protein.
Homo sapiens (human)
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/db_xref="G1:14424528"
//tb_xref="G1:14424528"
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//translation="Melltrgg"
//translation=
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Shevohenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Bendamin,B., Blakesley,R.W., Boufdard,G.G., Brinkley,C., Brooks,S.,
Bendamin,N.L., Guan,X., Gupta,J., Ho,S.-E., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GAGGAAGGAGCTCAGGGATATATACCGATCACAGAGTTTCAAAGGCGGAAACTATGCAGT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:14087 IMAGE:3927447"
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Contact: MGC help desk
Email: cgabs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
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llarity 99.9%; Pred. No. 1.5e-110;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="NICE-5 protein"
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Matches
     TITLE
JOURNAL
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ORIGIN
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COMMENT
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Euteleostomi;

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PRI 18-MAR-2001

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Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           1-808
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
Liu M., He F.;
Extractional prediction of the coding sequences of 121 new genes deduced
analysis of CDNA clones from human fetal liver";
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-DEC-1998) to the EMBL/GenBank/DDBJ databases.
Department of Experimental Hematology, Institute of Radiation Medicine,
Beljing Taiping Road 27, Beljing 100850, P. R. China
              2020 AACCCTTGCTAGCAGGCATTCTTATAAAAGAAACTTTCGAGCCTCCTTATATTGCTGGAA
   ACTCAGCTGTGCTCCAGACTAGAGCCTCCTTACCTATGGATTTTTAATTTTT
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/note="predicted protein of
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                                                                                                                                                                                                                                                                                                        63, Created)
67, Last updated, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/clone="FLC1398"
                                                                                                                                                                                                                                                                                                                                      sapiens PRO3094 mRNA, complete cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                           standard; RNA; HUM; 808
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Zhang C., Yu Y.,
Liu M., He F.;
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09-MAY-2001
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                                                                                                                                                                              /protein_id="CAB65097.1"
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Submitted (30-JUN-1999) Marenholz I., Universitaetsklinikum
Charite, Humboldt-Universitaet Berlin, Institut fuer Immungenetik,
Spandauer Damm 130, 14050 Berlin, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                keratinocytes"
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                                                                                                                                                                                                                                                                       243 t
                                       ρ
                                                                                                                                                                                                                                                                        180
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212. .427
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                                                                                                                                                                                                                                                            /gene="NICE-5"
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WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"NICE-5 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 20 Row: b Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8923743. Location/Qualifiers
                                                       Euteleostom1;
                                                                                                         Strausberg,R.

Direct Submission
Submitted (01-0CT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCCTTGGTGCAGATCCACGAAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAACTTTCCCTTTGACCCACCATTTGTCAGGGTTGTGTCTCCCAGTCCTCTCTGGAGGG
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 772)
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Pred. No. 3.9e-86;
0; Mismatches 0;
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/db_xref="LocusID:55585"
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/organism="Homo sapiens"
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llarity 100.0%; Pr
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/translation="MELLFKQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLT
RAQQSYKSLVQIHEKNGWYTPPKEDG"
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                                                                                        Score 794; DB 17;
Pred. No. 7.4e-89;
                                                                              35.2%; buc. 99.9%; pred. No. /...
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LOCUS DEFINITION

RESULT 14 BC015316

ACCESSION VERSION

1845	1905	1960 547	2015	2075	2135 721	2195 780	225 <b>4</b> 839
CCCTGGAGTATCACCCTTCCTCCCCCAGGCACCACTGGACCAATTACCTTTGAATGC	TGTATITIGGATCTCAGGCTGCTGTGGTTCCCTCCCTCATTITICTGGACGTGATAG	CTCTGCCTATTGCAGGACAATGATGGCTATTCTAAACGCTAAGGAAAAAAAA	ACACAGAACTGTTTCAAGTACTCAAGACTGACTTACAGACCAACCA	CTGGAACCCTTGCTAGCAGCATTCTTATAAAGAAACTTTCGAGCCTCCTTATATTGCT 	GGAAACTCAGCTGTGCTCCAGACTAGAGCTCCTTACCTATGCTATGGATTTTTAATTA 	TTTTCTCTTATTTCATGTACACTGCTTTTTTTGGTTACAGTGTATGATGGATG	aaaaatgtatctttgggaaaacaattacagtttgttaatttgaaaaaaaa
1786 370	1846	1906	1961	2016	2076	2136	2196
QY	Oy Db	Qy	QY	Qy	Qy	Qy Db	Oy . Db

Search completed: August 4, 2003, 19:04:22 Job time : 10669 secs

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August 4, 2003, 12:58:41; Search time 740 Seconds (without alignments) 8222.342 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                     2552756 seqs, 1349719017 residues
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Listing first 45 summaries
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/SIDS1/gcgdata/geneseg/genesegn-emb1/NA2002.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-emb1/NA2003.DAT:\* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT: /SIDS1/gcgdata/geneseg/genesegn-embl/NA1984.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-embl/NA1985.DAT:\*/SIDS1/gcgdata/geneseg/genesegn-embl/NA1986.DAT: /SIDS1/gcgdata/geneseq/genesegn-embl/NA1989.DAT: /SIDS1/gcgdata/geneseq/genesegn-embl/NA1990.DAT: /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2000.DAT geneseq/geneseqn-embl/NA2001B. /SIDS1/gcgdata/geneseq/genesegn-emb1/NA1988. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1982 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA199 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987 /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA19 geneseq/geneseqn-embl/NA /SIDS1/gcgdata/geneseq/geneseqn-emb] /SIDS1/gcgdata/geneseg/ /SIDS1/gcgdata, /SIDS1/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## UMMARIES

	Description	Human RATLId6 (red	Human colon cancer	Human prostate can	Human ORFX ORF2414	Human ORFX ORF1537	Novel human coding	Gene #3603 used to	Human gene signatu
	ΙD	AAD39359	AAH33115	AAZ33482	AAC76859	AAC75982	ABN59773	ABN97105	AAT19939
	ВО	24	22	20	21	21	24	24	16
	Length	2254	1666	1329	6277	791	. 2988	432	390
æ .	ywely re Match Length DB ID	100.0	0.69	59.0	52.0	31.9	20.5	19.2	16.5
	Score	2254	1554.4	1329	1172.4	720	461.2	432	371.4
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Human pancreatic t Human secreted pro Human reproductive Human reproductive Invertebrate forag DNA to infer human Human DNA to infer human Gene #2231 used to	0 1 H 2	Human differential Human colon cancer Human colon cancer Human colon cancer Drosophila melanog Drosophila melanog Gene #194 used to Colon adenocarcino Human endometrium Human differential Novel human polynu Human ovarian anti	EST clone C626. H Human breast cance Human colon tumour Nucleotide sequenc Mouse ribosomal RN Clone no. 161, sub Human prostate exp Bovine EST associa
AAD31836 AAC59573 AAL00214 AAL07355 AAD14006 AAD14299 AABNS5733	ABX11086 AA135089 AAV86232 AAD14005 AAD14208 ACC44721 ACC44629 AAZ52472	ABATTUGG ABH01601 ABH01601 ABH0058 ABL05399 ABB03696 ABL6216 AAA42109 AAH1515 AAF64725 ABL79430 ABL79430	AAV86060 AAL24217 ABL36952 AAV04906 ACC44633 ABX11090 ABV62051
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## ALIGNMENTS

AAD39359 standard; DNA; 2254 BP.

RESULT 1

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homologue, RATLIG6 (regulated in activated T-lymphocytes 1d6) and its corresponding nucleic acid. The invention also relates to methods for treating, diagnosing, preventing and screening for disorders related to the expression of RATLIG6: UBC is useful for screening for candidate computed scapable of binding to and/or modulating its activity. UBC is useful for treating an immune or neuronal disorder in a mammal. The method is useful for treating a cancer or tumour. It is useful for suppression the immune response in a subject requiring the suppression. It is also useful for treating lymphoproliferative disorder, cancer e.g. adenocarcinoma, lenkaemia, myeloma, sarcoma, etc, neurodegenerative disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma, multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's disease, dementia, depression, epilepsy, etc, immune disorder or immune related disorders such as acquired immuno deficiency syndrome (AIDS), alleay, anaemia, atopic dermatitis, diabetes mellitus, myocardial infarction, etc, developmental disorders e.g. Cushing's syndrome, renal infarction, etc, developmental disorders e.g. Cushing's syndrome, renal tresent sequence is human RATLIG6 gene.
                                                                                                                                                                                                                                                                                                          Novel ubiquitin conjugating enzyme polypeptide isolated from activated human T cell, for screening modulators useful for treating cancer, immune disorder, lymphoproliferative disorder, neurodegenerative
                                                                                                                                                                                                     Yang W, Finger
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 169pp; English.
                                                                                    30-OCT-2000; 2000US-244688P. 30-JUL-2001; 2001US-308706P.
                                           29-OCT-2001; 2001WO-US46559
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P-PSDB; AAE24493.
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Sequence 2254 BP; 547 A; 602 C; 648 G; 457 T; 0 other;

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                                 CTCGCTCCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
                                          GCTGACCCCCTTCGCGGGGGGATGCGTGTTTATCAGATCAAGACCAACCCGGTCAGC
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TTACCCACTCCCGGAGGTGGCGGCGCGCCATCTTGGCGAAGGGGGGATCAGGAAGTGCG
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and cancer antigens. The colon cancer antigens have cytostatic activity and cancer antigens. The colon cancer antigens have cytostatic activity and cancer in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with the prevention, or disease, associated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell of colorectal carcinomas and cancers. AAH37196 to AAH37204 and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH37789 represent sequences used in the exemplification of the
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                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
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NB. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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Matches 1572; Conservative
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P-PSDB; AAG73684.
28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) perioded by (A) are used. (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. Associated with known methods that use single (usually short) ESTs. Associated represent expressed sequence tags described in the method of the
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant, cardiant; immunositmulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antidianeamic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; catecarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsorlan; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinfammatory; antibacterial; antiviral; antifungal; antinheumatic; antitinfammatory; antibacterial; antiviral; antifungal; antinheumatic; the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malarla; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antlinflammatory disease; coagulation; thrombosis; contraceptive; ss.
 GTTACAGTGTATGATGGATGTATGAAAAAATGTATCTTTGGGAAAACAATTACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                   TCTCACCAAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTCAGTGATCATGCAGATCAG
                                                                                                                                                                                                                                                                                                                                        GCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCACGCTGCCTCTGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACCAACCAACCACCTTGCTGGAACCCTTGCTAGCAGGCATTCTTATAAAAGAAACTTT
                   TGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGTCAAACTCCTCAAAGTTGA
                             CATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGACCCACCATTTGTCAGGGT
                                                                                                                   CATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGACCCCACCATTTGTCAGGGT
                                                                                                                                      TGTGTCTCCAGTCCTCTGGAGGGTATGTTCTGGGCGGGGGGGCCATCTGCATGGAACT
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AAC75982
ID AAC7
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CGGAGGGGCCGGGGGGCCGGCCCGGACCGCATCTCCCCCCACGGGGGTCGGTGCC 

GCCCTGCCTGAGGCGAGAGCTGCTCGAGTCCATCTTCCACCGCGCCCACGAGCG

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Human; open reading frame; ORPX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiamatory; antitianaemic; gene therapy; cancer; proliferative antithyroid; antidiagemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; brocme denage; antilinflammatory disease; coaquiation;
                    Human ORFV ថាក្រាមនុក្ស polynucleotide sequence ទីមាន ព្រាសាលានេះលោក
                                                                                                                                                                                                thrombosis; contraceptive; ss
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB41773
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                                                                                                                                                                                                                     Homo sapiens
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303 AAAGAAAGGGAATACTCTGCTATTGCAGCATCTGAAGAGGATCATCTCCGACCTGTGTAA 362

990 ACTCTATAACCTCCCTCAGCATCCAGATGTGGAGATGCTGGATCAACCCTTGCCAGCAGA 1050 GCAGTGCACACAGGAAGACGTGTCTTCAGAAGATGAAGATGAGGAGATGCCTGAGGACAC 

930 AAAGAAAGGGAATACTCTGCTATTGCAGCATCTGAAGAGGATCATCTCCGACCTGTGTAA

243 CTGGTCGGTGGAGTCTGATGACCCTAACTTGGCTGCTGTCTTGGAGGCTGGTGGACAT

CTGGTCGGTGGAGTCTGATGACCCTAACTTGGCTGTTGTTTGGAGAGGCTGGTGGACAT

929 302 1109

1110 AGAAGACTTAGATCACTATGAAATGAAAGAGGAAGAAGCCAGCTGAGGGCAAGAAATCTGA 1169

542

1230 GCAAGATTACTTAAATGGTGCAGTGTCTGGCTCGGTGCAGGCCACTGACCGGCTGATGAA 1289

603 GCAAGATTACTTAAATGGTGCAGTGTCTGGCTCCAGGCCACTGACCGGCTGATGAA

1290 GGAGCTCAGGG---ATATATACCGATCACAGGTTTCAAAGGCGGAAACTATGC--AGTC 1344

663 GGAGCTCCAGGGATATATTACCGNTTCACAGGTTTCAAAGGCGGAAACTATGNCAGTTC 722

1345 GAACTCGT-GAATGACAGTCTGTATGATTGGAATGTCAAACTCCTCAAAGTTGACCAGGA 1403

723 GAACTCGTGGAATGACAGTCTGTATGGTTGGGATGTTCAACTCCTCAAAGTTGACCAGGG 782

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BP.

ABN59773 standard; cDNA; 2988

RESULT 6 ABN59773 28-JUN-2002

ABN59773;

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Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 791 BP; 198 A; 197 C; 234 G; 158 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 2293-2294; 5507pp; English.
                                                                       31-WAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-WAR-2000; 2000US-0540763.
31-MAR-2000; 2000WO-US08621
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; heaptortopic; vulnerary; sequences have activities such as: cytostatic; heartoprotective; cartiparkinsonian; nootropic; neuroprotective; manunostimilant; cardiant; thrombolytic; coagulant; vasotropic; munnostimilant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy proliferative disorders, neurodegenerative disorders, osteoarthritis, proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, humans, and the proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, humans, and the proteins and nucleic acids may be used to treat cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
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Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertiility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                          Novel human coding sequence SEQ ID NO: 184.
                                                                                                                                                                           expressed sequence tag; gene; ss.
                                                                                                                                                                                                           Homo sapiens
Gaps
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9
                                                                                                                                                      31.9%; Score 720; DB 21; Length 791; 97.1%; Pred. No. 2.6e-128; 1ve 0; Mismatches 17; Indels
                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 97.1
Matches 765; Conservative
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Sequence 432 BP; 138 A; 76 C; 93 G; 125 T; 0 other;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver tissue sample
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                WO200229103-A2.
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854
                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate he activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                            1077 AGAAGATGAAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCATCCTAGAGAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAATATTAGAGAAATTAGGAAGACTCAAAGGCAAGACCATTTAAATGGTGCAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCTCGGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGAAAGAAGGAGCCGACTTCATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                An isolated polynucleotide for treating diseases associated with its
                                                                                                                     Ren F;
                                                                                                                                                                                                                                                                                                                                                                                         Length 2988;
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                           encoded polypeptide such as cancer and multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                      Score 461.2; DB 24; Length
Pred. No. 1e-78;
0; Mismatches 158; Indels
                                                                                                                    Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2988 BP; 880 A; 587 C; 657 G; 864 T; 0 other;
                                                                                                                   Zhang J,
RT;
                                                                                                                                                                                                              Claim 1; SEQ ID NO 184; 509pp; English.
                                                                                                                   Asundi V,
', Drmanac
                                                                                                                   Zhou P, As
Wehrman T,
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                                                   .0-SEP-2001; 2001WO-US26015
                                                                       11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                 2002-292408/33
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                                                                                                                  Liu C,
Yang Y,
                                                                                             HYSE-) HYSEQ INC
                                                                                                                                                WPI; 2002-292408,
P-PSDB; ABB97360
          WO200222660-A2
                             21-MAR-2002.
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cytostasic activity. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                1215 ATCGGTCATCATGCAAATAAATGCCACCTTAGTCAAAGGCAAAGCCAGAGTGCAGTTTGG
                                                                                                                         1617 GTCAGTGATCATGCAGATCAGTGCCACACTGGTGAAGGGGAAAGCACGAGTGCAGTTTGG
                                                                                                                                                                                                                                                                                1677 AGCCAACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTTGGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene #3603 used to diagnose liver cancer.
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Score 432; DB 24; Length 432; Pred. No. 2.5e-73;

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7817 "CS" sequences given in AAr19001-T26873 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared if com a various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly!" as the sole primer. Since the 3'-end of mRNA by using poly!" as the sole primer. Since the 3'-end of mRNA by using poly!" as the sole primer. Since the 3'-end of mRNA hybridise with specific mRNAs Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200212327-A2
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                                                                                                                                           .936 TCTARACGCTRAGGRARARARCACAGACTGTTTCRAGTACTCARGACTGTT 1995
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                                                                                                                                                                                                                                                                                                                                2056 TCGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACTAGAGCCTCCTTACCTA
                            1816 GGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCACGCTGCCTCTGTGGT
                                                                                    1876 TCCCTCCCTCATTTTTCCTGGACGTGATAGCTCTGCCTATTGCAGGACAATGATGGCTAT
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                                            2116 IGCTATGGATTTTTAATTTATTTTCTCTTATTTCATGTACACTGCTTTTTTGGTTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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  Indels
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  Mismatches
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara K, Okubo K;
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(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-206931/27
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Matches 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                301 ACACTGCTTTTTTTTGGTTACAGTGTATGATGGATGTGTATGAAAAAAATGTATCGTTTGGG
                                                                                                                                            1854 GATCTCACGCTGCCTCTGTGGTTCCCTCCTCCATTTTTCCTGGACGTGATAGCTCTGCCT
                                                                                                   TCAAGTACTCAAGACTGACTTACAGACCAACCAACCACCTTGCTGGAACCCTTGCTAGCA
                                                                                                                                                                                                                                                                  GGCATTCTTATAAAAGAAACTTTCGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTC
                                                                                                                                                                                                                                                                                              GGCATTCTTATAAAAGAAACTTTCGAGCCTCCTTATATATGCTGGAAACTCAGCTGTGCTC
                                                                                                                                                                                                                                                                                                                           CAGACTAGAGCCTCCTTACCTATGCTATGGATTTTTAATTTTATTTTCTCTTATTTCATGT
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                                                          Gaps
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                          Score 371.4; DB 16; Length 390;
Pred. No. 9.6e-62;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human pancreatic tumour protein encoding cDNA clone 53803.2.
Sequence 390 BP; 109 A; 86 C; 67 G; 127 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2214 AAAACAATTACAGTTTGTTAATTTGAAAA 2243
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                          16.5%;
illarity 96.9%;
Conservative (
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P-PSDB; AAB34306
                                                                       W0200056883-A1
                                                    Homo sapiens.
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                                                                                                                                       23-MAR-1999;
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                                                                                              28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                       GCTGACCCCCTTCGCGGGGGGGATGCGTGCATTTATCAGATCAAGACCAACCCGGTCAGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides derived from pancreatic tumor cDNA library, useful as vaccines for preventing and treating pancreatic cancer, as well as for the diagnosis and monitoring of such cancers -
                                                                                                                                                                                                      of such
                                                                                                                                                                                                                                                                                                              1 CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
                                                                                                                                                                                                                                                                                                                        GGGCCGATCGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides derived from pancreatic tumour CDNA library, encoding pancreatic tumour proteins. The invention also relates to therapy and diagnosis of cancer, such as pancreatic cancer. The polypeptides and polynucleotides of the invention are useful as vaccines and pharmaceutical compositions for preventing and treating pancreatic cancer, as well as for the diagnosis and monitoring of such
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCCGATCGCACGCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynaecological; and antibacterial; gene therapy; detection; cancer; chromosome marker; chromosome identification; neural disorder; immune disorder;
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                                                                                                                                                                                                                                                                     DB 24; Length 870;
                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                             Sequence 870 BP; 221 A; 244 C; 221 G; 169 T; 15 other;
                                                                                                                                                                                                                cancers. The present sequence is human pancreatic
                                                                                                                                                                                                                                                                   Score 371.4; DB 2. Pred. No. 1.1e-61;
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                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                             Claim 1; Page 111; 120pp; English
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99.7%;
21-SEP-2000; 2000US-234451P
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                                                                                                                                                                                                                                                                                        372; Conservative
                                                             WPI; 2002-241738/29
                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                           encoding cDNA.
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human secreted proteins given in AAB34299 to AAB34347. AAB34348 to AAB34437 represent human secreted polypeptide sequences and proteins amonicogues to them, which are given in the exemplification of the present invention. Human secreted polypeptide sequences and proteins and calls the genes are expressed in Example of activities include: neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotroptc; muscular antiinfective; gynaecological; and antibacterial. The polynucleotides can be used for the detection of various disorders such as cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The secreted proteins can be used to treat disorders such as neural; immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wound healing, and infectious diseases. The proteins can
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   muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; wound healing; infectious disease; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also be used as a food additive or preservative to increase or decrease storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide sequences given in AAC59566 to AAC59614 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted proteins and gene sequences encoding them, useful for detecting, preventing, and treating disorders such as cancer, neurological disorders and immune system disorders -
gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the exemplification of the present invention
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0126054.
99US-0169916.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM,
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les 372; Conserv
                                                                                                         food additive; ss
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2000US-0249209
                                                      2000US-0231244
2000US-0231413
                                                                                 2000US-0231414
2000US-0232080
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                         08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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29-SEP-2000

20-CCT-2000

02-CCT-2000

13-CCT-2000

13-CCT-2000

20-CCT-2000

20-CC
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21 - SEP - 2000

25 - SEP - 2000

25 - SEP - 2000

27 - SEP - 2000

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27 - SEP - 2000

29 - SEP - 2000
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17 -NOV - 2000;
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  Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 8902.
                                                                                                                                              AAL06214/c
ID AAL06214 standard; DNA; 13076 BP.
                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01339
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2000US-0205515
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                                                               361 TTACCCACTCCCG 373
                                                                                 456 TTACCCACTCCCG 444
                                                                                                                                                                                                                21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                           WO200155320-A2
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14 - AUG - 2000;
14 - AUG - 2000;
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14 - AUG-2000;
18 - AUG-2000;
22 - AUG-2000;
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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05-SEP-2000;
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24-FEB-2000;
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                             Human reproductive system related antigen DNA SEQ ID NO: 10043
                        AAL07355 standard; DNA; 13076
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                                                                      (first entry)
                                                                                                                                                                          40200155320-A2.
                                                                                                                                                      Homo saplens
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1-AUG-2000
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                                                AAL.07355;
   RESULT 12
              AAL07355/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3452 GGGCCGATCGCACCCCCCGTGCCGACGACCATTCGAACGTCTGCCCTATCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CCCTCTCCGGCCCCGGGGGGGGGGGGCGCCGGCGCTTTGGTGACTCTAGATAACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 13076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13076 BP; 3078 A; 3655 C; 3680 G; 2643 T; 20 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.5%; Score 371.4; DB 22; Length Best Local Similarity 99.7%; Pred. No. 2.1e-61; Matches 372; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                      Ruben SM
                                                                                                                                                                                                                                              HUMA-) HUMAN GENOME SCI INC
                                                                                                      2000US-0251030.
2000US-0251988.
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                                                                                                                                        0000S-0251479
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2000US-0251990
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                                                                                             0000S-025039
                                                                                                                                                                                                                                                                      Barash SC,
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17 - NOV - 2000)
01 - DEC - 2000)
05 - DEC - 2000)
05 - DEC - 2000)
06 - DEC - 2000)
08 - DEC - 2000)
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29-SEP-2000;
02-OCT-2000;
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02-OCT-2000;
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                14-SEP-2000
                           21-SEP-2000
                                    26-SEP-2000
                                         7-SEP-2000
                   14-SEP-2000
                      L4-SEP-2000
                         -SEP-2000
                                 35-SEP-2000
                                                  29-SEP-2000
29-SEP-2000
                                                             -OCT-2000
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3452 GGGCCGATCGCACGCCCCCCGTGGCGCGACGACCATTCGAACGTCTGCCCTATCAACT 3393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3632 CTGGCTCCTCTCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CCCTCTCCGGCCCCGGGCGGGGGGGGCGCCGGCGCTTTGGTGACTTTGGTAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GGGCCGATCGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 13076;
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ABS65032
ID ABS65032 standard; DNA; 42999 BP.
XX
AC ABS65032;
XX
                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                2000US-0251030
2000US-0251988
                                                                                                                          2000US-0251989
2000US-0251990
                                                                                                                                                         11-DEC-2000; 2000US-0254097
05-JAN-2001; 2001US-0259678
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                                                                               2000US-0251856
                                                                                            2000US-0251868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein of the invention.
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01-DEC-2000, 2
05-DEC-2000, 2
05-DEC-2000, 2
05-DEC-2000, 2
06-DEC-2000, 2
08-DEC-2000, 2
08-DEC-2000, 2
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Translational regulatory element; internal ribosome entry site; IRES; cistron; protein stability; cell viability; protein yield; toxin; therapeutic agent; human; 18S ribosome; ds.
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/note= "2'-0-methyladenosine"
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509
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/note= "2'-0-methyladenosine"
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                                                                                                                                                                                                                                                            DNA to infer human 18S ribosomal RNA.
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                                                               4143 TTACCCACTCCCG 4155
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/mod_base=
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/mod_base=
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/mod_base=
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                                                361 TTACCCACTCCCG 373
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ID AAD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method of identifying a compound that modulates attention deficit hyperactivity disorder (ADHD) in a mammal. The method comprises administering a test compound to an invertebrate, and measuring a foraging behaviour of the invertebrate is characterised as a compound that modulates to the invertebrate is characterised as a compound that modulates. Of the invertebrate is characterised as a compound that modulates in a mammal. The compound identified by the new method of the invention is useful for diagnosing or treating ADHD, hypertension or other diseases associated with a nitric oxide/cMP-dependent protein distinguishes a compound that has a specific effect on ADHD, hypertension or other diseases associated with a compound that has a specific effect on ADHD, hypertension or other diseases associated with a mammal from a compound that has a non-specific effect. The present sequence represents a DNA sequence associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a compound that modulates an attention deficit hyperactivity disorder (ADHD) for treating e.g. ADHD or hypertension, comprises measuring a foraging behaviour an invertebrate -
 Invertebrate foraging behaviour associated human DNA sequence #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.5%; Score 371.4; DB 24; Length 42999; Best Local Similarity 99.7%; Pred. No. 2.7e-61; Matches 372; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 42999 BP; 6411 A; 13605 C; 11491 G; 11479 T; 13 other;
                            Attention deficit hyperactivity disorder; ADHD; hypertension; invertebrate foraging behaviour; nitric oxide; hypotensive; cGMP-dependent protein kinase; human; neuroleptic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 182-195; 246pp; English.
                                                                                                                                                                                                                                                                        (NEUR-) NEUROSCIENCES RES FOUND INC
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                                                                                                                                                                                                                                                                                                          Greenspan RJ, Shaw PJ;
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                                                                                                              Homo sapiens.
                                                                             gene therapy
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'note= "3-(3-amino-3-carboxypropyl)-
'methylpseudouridine"
                   'note= "2' -O-methyladenosine"
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The present invention relates to synthetic and isolated translational regulatory elements comprising oligonucleotides having translational enhancing activity, internal ribosome entry site (IRES) activity or translational inhibitory activity. The recombinant nucleic acid molecule of the invention comprises a synthetic translational regulatory element operatively linked to an expressible polynucleotide. The expressible polynucleotide comprises a first cistron encoding a polypeptide that enhances protein stability or cell viability, and a second cistron encoding a polypeptide of interest. The second cistron is operatively linked to the first cistron, and the expressible polynucleotide comprises an IRES element, which is operatively linked to the first cistron, or the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic translational regulatory element useful for altering translational activity, comprising oligonucleotides with translational regulatory activity and internal ribosome entry site activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
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12-JAN-2001; 2001US-0261312
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Best Local Similarity 99.5
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/note= 13-(3-amino-3-carboxypropyl)-
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mod_base= OTHER
fnote= "2'-O-methyladenosine"
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                                                                                                                                            Transcriptional regulatory element; translational regulatory element; gene expression; diagnostic application; therapeutic application; human; ribosomal RNA; 18S rRNA; internal ribosome entry site; IRES; ds.
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Identifying oligonucleotides with transcriptional/translational regulatory activity in eukaryotic cells by integrating an oligonucleotide into cell genome and detecting a change in expression of expressible polynucleotides -
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Meech R;

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The present invention relates to a method for the identification of an oligonucleotide with transcriptional/translational regulatory activity an eukaryotic cell. The method involves integrating an oligonucleotide into the genome of an eukaryotic cell so that it is linked to an

Example 7; Page 167-168; 172pp; English.

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expressible polynucleotide or contacting the eukaryotic cell with library of vectors, obtained by cloning a library of oligonucleotide into multiple copies of expression vectors comprising polynucleotide, and detecting changes in expression of the polynucleotide. The method is useful for identifying an oligonucleotide having transcriptional or translational activity in a eukaryotic cell. It is also useful for identifying synthetic transcriptional or translational regulatory elements. The transcriptional or translational regulatory elements are
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Pred. No. 2.7e-61;
0; Mismatches 2; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 29, 2003, 13:47:14 ; Search time 52 Seconds (without alignments) 963.781 Million cell updates/sec

US-10-005-549-2 2229 1 MQPQPQGQQQQPGQQLGG......KSLVQIHEKNGWYIPPKEDG 422 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

451899 seqs, 118759770 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

ptodata/2/pubpaa/US10a\_PUBCOMB.pep:\* ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\* Ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\* //ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\* //ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\* PUBCOMB.pep:\* /ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\* ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*/Cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:#/cgn2\_6/ptodata/2/pubpaa/PCT\_NRW\_PUB.pep:#/cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:#/cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:#/cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:# ptodata/2/pubpaa/US10C\_ Published\_Applications\_AA:\* /cgn2\_6/ptodata/2/cgn2\_6/ptodata/ /cgn2\_6/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4458, Ap	Sequence 4, Appli	Sequence 8352, Ap	Sequence 3352, Ap	Sequence 5, Appli	Sequence 10088, A Sequence 5676, Ap	Sequence 1083, Ap	Sequence 216, App	Sequence 216, App	Sequence 216, App	Sequence 3, Appli
SUMMARIES	US-10-106-698-4458 US-09-864-761-43956	US-09-842-528-4 US-10-060-019-22	US-10-128-714-8352	US-10-128-/14-3352 US-10-174-363-56	US-09-842-528-5	US-10-130-/01-10088 US-09-738-626-5676	US-09-925-301-1083	US-09-738-973-216	US-09-854-133-216	US-10-144-649A-216	US-09-742-096-3
DB	15	9	13	15	9 5	101	σ	10	10	12	10
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Score	1863	137 135.5	134.5	122.5	121.5	120.5	119.5	118	118	118	116.5
Result No.	40	m 4•	ın u	۰,	<b>∞</b> σ	10	I :	12	13	14	15

16         5.2         1647         11         US-09-824-574-4         Sequence 4, Appliance 2, Appliance 2, Appliance 31, Appliance 32, 112.5         5.0         161         9         US-09-925-297-801         Sequence 4, Appliance 31, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 33, Appliance 34, Ap																															
5.2 1647 5.1 1569 5.0 1647 5.0 1647 5.0 1647 5.0 1647 5.0 1647 5.0 1647 5.0 1647 6.8 1648 6.8 1648 6.9 1648 6.9 1648 6.9 1648 6.0		Sequence 4, Appli	Sequence 31, Appl	Sequence 2. Appli	Sequence 401. App	Sequence 801, App	Sequence 292. App	Segmence 406. App	Sequence 7, Appli	Sequence 331. App	6			Sequence 294. App	Sequence 408, App	Seguence 4. Appli	Sequence 4. Appli	Sequence 4, Appli	Seguence 412. App	Sequence 399, App	Sequence 2, Appli	Sequence 1002, Ap	Sequence 1002, Ap	Sequence 392, App	Sequence 324, App	Sequence 8314, Ap	Sequence 56, Appl	Sequence 2, Appli	Sequence 150, App	Sequence 2, Appli	Sequence 2, Appli
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		104/	265	519	176	161	147	147	525	147	1084	592	592	147	147	148	148	148	156	143	641	647	647	143	462	1070	510	151	151	758	758
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0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	711	OTT .	115.5	114	113.5	112.5	111.5	111.5	111.5	109.5	109	108	108	107.5	107.5	107.5	107.5	107.5	107	106.5	106.5	106.5	106.5	105.5	105.5	105.5	105	104.5	104.5	103.5	103.5
		91	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

US-10-106-698-4458

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REPRENCE: PAGOSPI
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-109-39
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PALENTIN VOICE: 3.0 COTION: (25)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC\_FEATURE

LOCATION: (38)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-4458 Sequence 4458, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION: TYPE: PRT ORGANISM: Homo sapiens NAME/KEY: MISC\_FEATURE SEQ ID NO 4458 LENGTH: 374 FEATURE:

Gaps ö Length 374; Indels 83.6%; Score 1863; DB 15; 98.4%; Pred. No. 3.1e-132; tive 0; Mismatches 6; Query Match 83.6 Best Local Similarity 98.4 Matches 358; Conservative

59 FRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCNITESYPAVPPI 118 

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307 KEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQG----- 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EGGVF-KLEIEFPEDYPFKPPKVRFTSKIFHPNIYSNTGRICLDILKDPGDDPNGYE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 EDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Meyers, Rachel A.
APPLICANT: Meyers, Rachel A.
APPLICANT: Tsai, Fong Ying
TITLE OF INVENTION: 27960, A NOVEL UBIQUITIN CONJUGATING
TITLE OF INVENTION: ENZYME FAMILY MEMBER AND USES THEREFOR
FILE REFERENCE: 10448-045001
CURRENT APPLICATION NUMBER: US/09/842,528
CURRENT FILING DATE: US 60/199,500
PRIOR APPLICATION NUMBER: US 60/199,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EDLDHCEMK-EEPTSEKKLEDEGTEKENWAILEKIRKTERQGHLN 45
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                                                                                                                                                                                                                                                                     INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3
INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.3
INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.2
INFORMATION: SWISSPROT HIT: PO2547, EVALUE 2.100+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 140.5; DB 9;
Pred. No. 0.00073;
4; Mismatches 10;
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 43956
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: consensus sequence US-09-842-528-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 ----WSSAYSIESVIMQISATL 377
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; Sequence 22, Application US/10060019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09842528 Patent No. US20020004236A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3%;
Best Local Similarity 66.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO ACCOUNER INFORMATION: EXPRESSED
                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
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TLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                    LHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                      GWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIHEKNGWYTPP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                WSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPLPAE 178
                                                                                                                          QCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00668 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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RIOR FILING DATE: 2000-02-04
RIOR APPLICATION NUMBER: US 60/207,456
RIOR APPLICATION NUMBER: US 09/632,366
RIOR APPLICATION NUMBER: GS 09/632,366
RIOR FILING DATE: 2000-08-03
RIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43956, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 KEDG 422
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus an
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-23
PRIOR PLILNG DATE: 2001-04-23
PRIOR PLILNG DATE: 2001-04-05
PRIOR PLILNG DATE: 2001-06-05
PRIOR PLILNG DATE: 2001-06-05
PRIOR PLILNG DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-03
                                                                                                                                                                                                                                                                         276 VELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVV 335
                                                                                                                                                                                                                                                                                                                                                                                                                              336 SPVLSGGYVLGGGAICMELLTKQG------WSSAYSIESVIMQISATL----VK 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 LYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGG 342
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                                                                                                                                                                                                                                                                                                                21 IELNDEDIFNWANGLIVLANDSLYY-----GGYFKASMKFSKNYPYSPPEFRFL
                                                                                                                                                                                                                     33;
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                                                                                                                                                           Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
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                                                                                                                                                                                                                        Indels
                                                                                                                                                           ; DB 15;
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                                                                                                                                                                                                                  28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                           Score 134.5;
Pred. No. 0.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 GKARVQFGANKSQYSLTRAQQSYKSLVQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%; Score 133; Best Local Similarity 21.9%; Pred. No. 0 Matches 44; Conservative 35; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3352, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 GANKSQYSLTRAQQSYKSLVQ 407
            ; LENGTH: 223
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Aspergillus fumigatus US-10-128-714-3352
                                                                                                                                                        Query Match 6.0%;
Best Local Similarity 25.0%;
Matches 37; Conservative 2
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Tishkoff, Daniel
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YENDERAL INCOMPANTATION:

APPLICANT: Hu, Wengi

APPLICANT: Tishofoff, Daniel

APPLICANT: Tishofoff, Daniel

APPLICANT: Tishofoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Enoshkin, Alexey M

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Indentification of Essential Genes in Aspergillus funigatus and

TITLE OF INVENTION: Methods of Use

FILE REPREBUCE: 10182-018-99

CURRENT PILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR APPLICATION NUMBER: US 60/285,890

PRIOR FILING DATE: 2001-04-27

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-05

PRIOR RELING DATE: 2001-08-31

WUMBER OF SEQ ID NOS: 8603

SOFWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 NINSPANVDAAVDYRKNPEQYKQRVKMEVERSKQDIPKGFIMPTSESAYISQSKLDEPES 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 NYAVELVNDS-LYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPF 331
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                                          Subtract in Communication:

APPLICANT: Tyers, Milem
APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.100501
CURRENT APPLICATION NUMBER: US/10/060,019
CURRENT APPLICATION NUMBER: US/09/177,165
PRIOR APPLICATION NUMBER: US/09/177,165
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1997-10-24
SPIOR FILING DATE: 1997-10-24
SOFTWARE: PALENTION NUMBER: 60/063,254
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 22
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 VRVVSPVLSGGYVLGGGAICMELLTKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8352, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Saccharomyces cerevisiae US-10-060-019-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KNGWYTPPKED 421
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Publication No. US20030003564A1 GENERAL INFORMATION:
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------GPGGGGGGFAGRPGGPGGGGGRPGFGGRPGG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TPYEGGVF 46
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Best Local Similarity 21.3%; Pred. No. 1.4;
Matches 98; Conservative 44; Mismatches 164; Indels 155; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 144;
TITLE OF INVENTION: 27960, A NOVEL UBIQUITIN CONJUGATING TITLE OF INVENTION: ENZYME FAMILY MEMBER AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 121.5; DB 9; Best Local Similarity 26.8%; Pred. No. 0.093; Matches 33; Conservative 27; Mismatches 46;
                       TITLE OF INVENTION: ENZYME FAMILY MEMBER AN FILE REFERENCE: 10448-045001
CURRENT APPLICATION NUMBER: US/09/842,528
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,500
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10088
LENGTH: 1046
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APPLICANT: HORIKAWA, HURSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATYORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: consensus sequence US-09-842-528-5
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Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                        Squence 56, Application US/10174363

Publication No. US20030077623A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Butler, Karlene H.
APPLICANT: Barvell, Leslie T.
APPLICANT: Refalski, Antoni J.
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Gene Silencing
FILE REFERENCE: BB1434 US. NA
CURRENT APPLICATION NUMBER: US/10/174,363

CURRENT FILING DATE: 2002-06-17

PRIOR PELING DATE: 2000-06-18

PRIOR FILING DATE: 2000-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 GIGKENLAILEKIKKNQRQDYLNG---AVSGSVQATDRLMKELRDIYRS--QSFKGGNYA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 ----VNRAVMKQLVDNYRDSHLGSRLPAYDGR------KSLYTAGPLPFNSKEFR 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 FILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAY-SIESVIMQ 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 PQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYE--MKEEEPAEGKKSEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PMRP-----GKGOSGKRCI---VKANHFFAELPD--KDLHHYDVTITPEVTSRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15; Length 1048;
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| | | : :|||:||:
| GV-----MLRKDFESYKALVR 166
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372 LSLNIDMSSTAFIEANPVIQF 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana US-10-174-363-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 56
SOFTWARE: Mccrosoft Office 97
SEQ ID NO 56
LENGTH: 1048
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APPLICANT: Meyers, Rachel A.
APPLICANT: Tsai, Fong-Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-842-528-5
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OY 141 GNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQED	; Sequence 1083, Application US/09925301 ; Patent No. US20020052308A1 ; GRMERAL INFORMATION:     APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies     FILE REFERENCE: PA106     CURRENT APPLICATION NUMBER: US/09/925,301     CURRENT APPLICATION NUMBER: US/09/925,301     CURRENT PILING DATE: 2001-08-10     PRIOR APPLICATION NUMBER: 60/124,270     PRIOR APPLICATION NUMBER: 60/124,270     PRIOR PILING DATE: 1999-03-12     NUMBER OF SC ID NOS: 1694     SOFTWARE: PATENTIN Ver. 2.0     SOFTWARE: Homo sapiens     FEATURE:     NAME/KEY: SITE     LOCATION: (56)     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids     US-09-925-301-1083	Ouery Match 5.4%; Score 119.5; DB 9; Length 256;  Best Local Similarity 22.9%; Pred. No. 0.29;  Matches 49; Conservative 32; Mismatches 96; Indels 37; Gaps 8;  Qy 187 SEDEDEMPEDTEDLHYEMKEEEPAEGKKSEDGIGKENLAILEKIKKNQRODYLNGAV 246    1	247 SGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLXDWNVKLLKVDQDSALHNDLQIL  :              ::   ::     :::   114RIQKELADITLDPPPNCSAGPKGDNIYEWRSTILGPPGSVY	307 KEKEGADFILLNRSFKDNRPPEDPFVRVVSPVLSG 	DD 209 SKVLLSICSLITDCNPADPLVGSIATOYMINRAE 242 RESULT 12	US-09-738-973-216 ; Sequence 216, Application US/09738973 ; Patent No. US20020110563A1
09   06   09   09   09   09   09   09		PRIOR FILING DATE: 2000-04-07  PRIOR APPLICATION NUMBER: JP 00/280988  PRIOR FILING DATE: 2000-08-03  NUMBER OF SEQ ID NOS: 7059  SOFTWARE: PATENTIN VET. 3.0  SEQ ID NO 5676  LENGTH: 1004  TYPE: PRT  TYPE: PRT	core 120.5; DB 10; Length 1004;	. A-d	34 GPGPGPCLRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPP	QY 94 RGSVPGDPVRIHCNITESYPAVPIWSVESDDPNLAAVLERLVDIKK 140

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                                                  APPLICANT: Fling, Steven r.,
APPLICANT: Mohamath, Raodoh
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Banlot, Mark
APPLICANT: Manlot, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
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22.3%; Pred. No. 1;
tive 33; Mismatches 141; Indels 150;
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APPLICANT: Mohamath, Raodoh
APPLICANT: Mohamath, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
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Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
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Best Local Similarity 22.35
Matches 93; Conservative
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for 8
SEQ ID NO 216
LENGTH: 527
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; ORGANISM: Homo sapien
US-09-738-973-216
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C11
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                                                                                                                                                                                                                       ; Pred. No. 1;
33; Mismatches 141;
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CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFWARE: FastSEQ for Windows, Version 3.0
SEQ ID NO 216
LENGTH: 527
TYPE: PRT
                                                                                                                                                                                                  5.3%; Score 118; 22.3%; Pred. No. 1
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Matches 93; Conservative
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US-10-144-649A-216
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US-09-854-133-216
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Best Local Similarity
Matches 93; Conserv
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US-10-144,649A-216
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                                                                                                                                                                                               --- QPLPAEQCTQEDVSSEDEDEEMPEDT 198
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                                            220 PPEAOPRRIEPAPPRA--RPEVAPEGEPGAPDSRAGGDTALSGDGDPRPERKGPEMPRI 277
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CLRRELKLLESIFHRGHERFRIA----SACLDELSCEFLLAGAGGAGGAAPGPHLP-- 92
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TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
TILLE REFERENCE: 200773US0DIV
CURENT APPLICATION NUMBER: US/09/742,096
CURRENT FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: US 08/973,642
PRIOR FILING DATE: 1998-02-06
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                                                                                                                             5.2%; Score 116.5; DB 10;
25.7%; Pred. No. 6.8;
tive 36; Mismatches 79;
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PRIOR FILING DATE: 1996-06-12
PRIOR APPLICATION NUMBER: FR 95/07007
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Patent No. US20020155441A1
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
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Best Local Similarity 25.7%
Matches 58; Conservative
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APPLICANT: DRUILHE, PIERRE
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US-09-742-096-3
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LENGTH: 1786
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Search completed: July 29, 2003, 13:56:17 Job time : 54 secs

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/1/ina/PcTUS.COMB.seq:\*
6: /cgn2\_6/ptodata/1/ina/PcTUS.COMB.seq:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 193, App			Sequence 952, App		178,	281,	19,	13	13	19	13	13	19	13	'n	7	4	25	25	Sequence 25, Appl	25,	25	25,	25,	27	7	
SUMMARIES	ΩI	US-09-397-787-193	US-08-867-820A-1	US-08-093-144-6	US-08-998-416-952	US-09-350-710B-1	US-08-998-416-178	US-08-998-416-281	US-08-967-101-19	92-541-1	-698-1	27-480-1	841C-	US-09-124-523-19	US-09-636-796A-19	Ţ	144-	371-	-093	-87	-87	US-07-879-470A-25	-87	-87	-87	-879	-07-879-647A-	US-07-879-584A-27	
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	Score	169	140.8	140.6	137.2	137.2	136.8	136.6	135.4	135.4	135.4	135.4	135.4	135.4	135.4	135.4	133.8	130	128.2	126.6	126.6	126.6	126.6	126.6	126.6	126.6	126.6	126.6	,
	Result No.		7	e	Ω 4	c 2	9 0	-	υ O		-	-	-	Н.	_	7	16	17	18	19	20	21	22	23	24	25	26	27	

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Sequence 1, Application US/08867820A Patent No. 5891685 GENERAL INFORMATION: APPLICANT: YAMAGISHI Masahiro APPLICANT: TAKAI YUKIE

RESULT 2 US-08-867-820A-1

Appl Appl Appl Appl Appl Appl Appl Appl		0;
REFEREREEEEEEEEE	,	ũ
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07-879-470A-2 07-879-644A-2 07-879-644A-2 07-879-594A-2 08-093-144-8-2 08-093-144-8-2 07-879-647A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2 07-879-64A-2	, metho	re 169; D ed. No. 4e Mismatches
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US-07-879-470A-27 US-07-879-644A-27 US-07-879-594A-27 US-07-879-464A-27 US-08-09-144-8-24 US-07-879-647A-24 US-07-879-644A-24 US-07-879-644A-24 US-07-879-644A-24 US-07-879-644A-24 US-07-879-644A-24 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26 US-07-879-644A-26	1397787	Score 169; Pred. No.
A S C C C C C C C C C C C C C C C C C C	09397 LONS HERAN 16 S Ve.	°° ;
ананананананан	787-193 193, Application US/09397787 187. 6468758 INFORMATION: NT: Lodes, Michael J. NT: Lides, Michael J. NT: Mitcham, Jennifer L. NT: Mitcham, Jennifer L. NT: King, Gordon E. NT: King, Gordon E. TIVENTION: COMPOSTITIONS AND METHODS FOR FE INVENTION: COMPOSTITIONS AND DIAGNOSIS FERENCE: 210121.466c2 APPLICATION NUMBER: US/09/397,787 FILING DATE: 1999-09-16 OF SEQ ID NOS: 334 FE FastSEQ for Windows Version 3.0 0 193 SM: Homo sapien E: SM: Micc. feature ON: (1) (477) INFORMATION: n = A,T,C Or G	7.5%; 100.0%; ive
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1749 1749 1749 1749 1749 1748 1748 1748 1750 1750 1750 1750	3, Application US/(648758 ORMATION: Benson, Darin R. Lodes, Michael J. Mitcham, Jennifer King, Gordon E. KING, Gordon E. NVEWTION: COMPOSITI NVEWTION: COMPOSITI NVEWTION: COMPOSITI NVEWTION: COMPOSITI NVEWTION: COMPOSITI NVEWTION: OMDER: ULICATION: UNDER: 210121.466C2 ENCE: 210121.466C2 ENCE: 210121.466C2 ENCE: 210121.466C2 ENCE: 210121.466C2 FESTESEQ for Windows 37 HOMO Sapien misc_feature (1)(477) ORMATION: n = A,T,(-193)	7. larity 100 Conservative
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	7-78 NO. 10 NO. 1 L INNO. CANT CANT CANT CANT NT AR NO. OF NO. NO. NO. NO. NO. NO. NO. NO. NO. NO.	Mat oca s
200mmmmmmmm444444 80010m4m9pcs010m44	RESULT 1  US-09-397-787-193  Sequence 193, Application US/ Patent No. 648878  APPLICANT: Benson, Darin R. APPLICANT: Lodes, Michael J. APPLICANT: Mitcham, Jennifer APPLICANT: Mitcham, Jennifer APPLICANT: Mitcham, Gondon E. TITLE OF INVENTION: COMPOSIT TITLE OF INVENTION: COMPOSIT FILE REFERENCE: 210121.466C2 CURRENT FILING DATE: 1999-09 NUMBER OF SEQ ID NOS: 334 SOFTHARE: FastSEQ for Window SEQ ID NO 193 LENGTH: 477 TYPE: DNA QRGANISM: Homo sapien FEATURE: NAMMEKKEY: Misc_feature LOCATION: (1)(477) OTHER INFORMATION: n = A,T,	Query Match Best Local Similarity Matches 169; Conser
01 01 01 01 01 01 01 01 01 01 01 01 01 0	RESULT Seque Seque GENE APP APP APP APP APP APP APP APP APP AP	Que Bes Mat
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287 TGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCGATAC 346
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 140.6; DB 1;
Pred. No. 8.1e-18;
0; Mismatches 34;
Eleventh Floor, 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                NAME: Hymo, Lawrence A.
REGISTATION NUMBER: 19,057
REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: No. 6239264art1s Corporation
: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,192
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-998-416-952/c; Sequence 952, Application US/08998416; Sequence 952, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION:
                                                                                                   MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.2%;
Best Local Similarity 82.6%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 444 base pairs
TYPE: nucleic acid
                                ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Tene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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ADDRESSEE: NO. 623920
STREET: 3054 Cornwall
CITY: Research Trian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double
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                   Washington
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                   APPLICANT: OHARA AKIKO
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S)- -HALOGENATED- -HYDROXXBUTY
NUMBER OF SEQUENCES: 57
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Patent No. 5434048
GENERAL INFORMATION:
APPLICANT: SIMON, LUC
APPLICANT: LALONDE, MAURICE
TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 6.2%; Score 140.8; DB 2
Best Local Similarity 76.8%; Pred. No. 1.1e-17;
Matches 172; Conservative 0; Mismatches 55
                                                                                                                        SEE: WENDEROTH, LIND & PONACK, L.L.P. 2033 K Street, N.W., Suite 800 Washington, D.C.
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA PROBES FOR THE TITLE OF INVENTION: ARBUSCULAR ENDOMYC NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENTA

NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-820
""" FFAX: 202-721-820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
STRAIN: MUCL29800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
 MIKAWA Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
                   HARA Mari
UEDA Makoto
                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSEE: WENDEROTH
                                                                                                                                                                                                                                                                                                                                                FILING DATE: Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                      USA
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                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-093-144-6
APPLICANT:
                                                                                                                                                STREET:
                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
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150 GCCGGCGCCTTTGGTGACTCTAGATAACCTCGGGCCGATCGCACGCCCCCCTGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                      210 ACGACCCATTCGAACGTCTGCCCTATCAACTTTCGATGGTAGTCGCCGTGCCTACCATGG
                                                                                                                                                                                            Gaps
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0
                                                                                                                          Length 1776;
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Steiner, Sabine
Mohr, Christine
Mendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
VEWTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1370 CCACATCCAAGGAAGCAGCAGGCGCGCAAATTACCCAATCC 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 CCACATCCAAGGAAGGCAGCAGCGCGCAAATTACCCACTCC 371
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MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: CH 0016/97
FILING APPLICATION NUMBER: APPLICATION: ANALY APPLICATION NUMBER: APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                    Score 137.2; DB (
Pred. No. 5.1e-17;
                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 178, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: POLIMBON, Peter
APPLICANT: Pohlmann, Rainer
                                  ORGANISM: Yeast integration vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                          6.1%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-998-416-178/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                        US-09-350-710B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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Patent No. 648918
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Hendrick, Carol A.
APPLICANT: Ruser, Barbara G.
APPLICANT: Ruser, Barbara G.
APPLICANT: Hogenson, Dean A.
TITLE OF INVENTION: Stability of Silage
FILE REFERENCE: Killer yeast
CURRENT APPLICATION NUMBER: US/09/350,710B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 GICTICGGACICTITGAIGATICATAATAACTITICGAAICGCAIGGCCTIGICCIGGCG 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 GCCGGCGCTTTGGTGACTCTAGATAACCTCGGGCCGATCGCACGCCCCCCGTGGCGGCG
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                                                                                                                                                                                                                        SOFTWARES: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 31-DEC-1996
ATTORNEY/AGBNT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 137.2; DB Pred. No. 4e-17; 0; Mismatches
                                                                                                                                                                                                            PC-DOS/MS-DOS
                  6239264th Carolina
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 952: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.1%;
Best Local Similarity 76.1%;
Matches 169; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919-541-8689
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: PAG1588UP
US-08-998-416-952
No. o
USA
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                                                                                                                                           197 CCCCGTGGCGGCGACGACCATTCGAACGTCTGCCCTATCAACTTTCGATGGTAGTCGCC
                                                                                                                                                                                                                         257 GTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCC
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                        317 TGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCC 371
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                                                           Length 709;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 7.3e-17;
0; Mismatches 1
                                                           Score 136.6; DB 3
Pred. No. 5.1e-17;
0; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TESTA, HURWITZ & THIBEAULT
gh Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
FILING PATE: 10-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08967101 Patent No. 5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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ilarity 86.3%;
Conservative
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Best Local Similarity 98.77
Matches 147; Conservative
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ADDRESSEE: TESTA, HU
    PAG1237UP
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                                                             Query Match
Best Local Similarity
Matches 151; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-967-101-19/c
  ; ORGANISM:
US-08-998-416-281
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                                                                                                                                         150 GCCGCCGCCTTTGGTGACTCTAGATAACCTCGGGCCGATCGCACGCCCCCCTGGCGGCG
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APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Renechtle, Philipp
APPLICANT: Relection of Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE: 1152
CORRESPONDENCE ADDRESS:
                                                           Length 703;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                             274 CCACATCCAAGGAAGGCAGCAGCGCGCAAATTACCCAAWCC 233
                                                                                                                                                                                                                                                                                                                                                                                      330 CCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCACTCC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF/5-30306/A/CGC1976
                                                           Score 136.8; DB 3 Pred. No. 4.7e-17;
                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: No. 6239264artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGRNT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 281, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPĖ: DNA (genomic)
ORIGINAL SOURCE:
                                                      Best Local Similarity 75.7%;
Matches 168; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919-541-8689
  PAG1070RP
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; ORGANISM:
US-08-998-416-178
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COMPUTER READABLE FORM:
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                                                                                                                                       STATE: MA
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      APPLICANT:
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                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: SOMMENS, JOHANNA M
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS J
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 7.3e-17;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: High Street Tower - 125 High Street CITY: Boston
                                                345 GCAGCAGGCGCGCAATTACCCACTCCCG 373
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                                                                   60 GCAGCAGGCGCGCAAATTACCCACTCCCG 32
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APPLICANT: ST. GEORGE-HYSLOP, PETER
APPLICANT: ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                   Sequence 19, Application US/08592541
Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09124698
Patent No. 6117978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 98.73
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
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US-09-124-698-19/c
                                                                                                                                                 US-08-592-541-19/c
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285 GGGAATCAGGGTTCGATTCCGGAGGGAGCCTGAGAAACGGCTACCACATCCAAGAAG 344
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CORRESPONDENCE S: 183
ADDRESSEE: TASTRA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
    GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                            & THIBEAULT
- 125 High Street
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Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pitcher, Edmund R. TELECOMMUNICATION:
                                                                                              ESTA, HURWITZ
High Street Tower
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TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
TITLE OF INVENTION: GENE
TITLE OF INVENTION: TO A
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURV
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STATE: Massachusetts
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                                                                                                                 STREET: High
CITY: Boston
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Gaps

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us-10-005-549-1.rni

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180 TCTGCCCTATTAACTTTCGATGGTAGTCGCCGTGCCTAACCATGGTGACCACGGGTGACG 121
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                                                                                                                                                                                                                                                            Length 395;
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APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
                                                                                                                                                                                                                                                          Score 135.4; DB 3;
Pred. No. 7.3e-17;
0; Mismatches 1;
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STREET: High Street Tower - 125 High Street
CITY: Boston
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                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-496-841C-19
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APPLICATION NUMBER: US/08/592,541
FILING DATE:
    TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-124-523-19/c
; Sequence 19, Application US/09124523
; Patent No. 6395960
                   INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                       6.0%;
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.7<sup>1</sup>
Matches 147; Conservative
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STRANDEDNESS: single
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 GGGAATCAGGGTTCCAATTCCGGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 135.4; DB 3;
Pred. No. 7.3e-17;
0; Mismatches 1;
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                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 395 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Paul F. Fehlner, Ph.D. REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 19, Application US/08496841C

Patent No. 6210919

GENERAL INFORMATION:
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ADDRESSEE: Darby & Darby,
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 98.7%;
Matches 147; Conservative
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345 GCAGCAGGCGCGCAAATTACCCACTCCCG 373
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Best Local Similarity 98.7'
Matches 147; Conservative
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                                                                         226 TCTGCCCTATCAACTTTCGATGGTAGTCGCCGTGCCT-ACCATGGTGACCACGGGTGACG 284
                                                                                                                   121
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                                                                                                                                                                                           19
                                                                                                                                                                         120 GGGAATCAGGGTTCCATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAG
                                                                                                               180 TCTGCCCTATTAACTTTCGATGGTAGTCGCCGTGCCTAACCATGGTGACCACGGGTGACG
                                           Gaps
                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
     Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/09/636,796A
FILING DATE: 11-A04-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
Score 135.4; DB 4;
Pred. No. 7.3e-17;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

6.0%; Score 135.4; DB 4;
Best Local Similarity 98.7%; Pred. No. 7.3e-17;
Matches 147; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/592,541 FILING DATE: <Unknown>
                                                                                                                                                                                                                               345 GCAGCAGGCGCGCAAATTACCCACTCCCG 373
                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-636-796A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09636796A Sequence 10, Application US/09636796A Patent No. 6485911 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
Query Match 6.0%;
Best Local Similarity 98.7%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                     US-09-636-796A-19/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 GGGAATCAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GGGAATCAGGGTTCGATTCCGGAGGGGGGCCTGAGAAACGGCTACCAAGGAAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 TCTGCCCTATCAACTTTCGATGGTAGTCGCCGTGCCT-ACCATGGTGACCACGGGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
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Pred. No. 7.3e-17;
0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,048F
FILING DATE: 28-Apr-1995
CLASSIFICATION: <unimnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: FEHLMER, PAUL F.
REGISSTRATION UMBER: 35135
REFERENCE/DOCKET NUMBER: 1034/0F808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 GCAGCAGGCGCGCAAATTACCCACTCCCG 373
60 GCAGCAGGCGCGCAAATTACCCACTCCCG 32
                                                                                                                                                                                                                 PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GCAGCAGGCGCAAATTACCCACTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DARBY & DARBY P.C. STREET: 805 THIRD AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-527-6237
                                                                                                       US-08-431-048F-19/c; Sequence 19, Application US/08431048F; Patent No. 6531586; GENERAL INFORMATION:
                                                                                                                                                                                                              APPLICANT: ST. GEORGE-HYSLOP,
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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us-10-005-549-1.rnpb

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic search, using sw model OM nucleic

August 4, 2003, 16:06:37; Search time 652 Seconds (without alignments) 7131.908 Million cell updates/sec Run on:

US-10-005-549-1 2254

Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1439767 segs, 1031500376 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

## STIMMARTES

						SUMMARIES	
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Result	ı,		Query				•
~ ;	. i	Score	Match	Match Length DB	DB	Ü	Description
υ	Н	1554.4	69.0	1666	14		Sequence 181. Apr
O	~	432	19.2	432	10	US-09-880-107-3600	Sequence 3600. Ar
	m	371.4	16.5	870	10	US-09-919-344-14	
O	4	371.4	16.5	13076	11	US-09-764-891-8902	Sequence 8902. At
ပ	2	371.4	16.5	13076	11	US-09-764-891-10043	Sequence 10043
	9	371.4	16.5	42999	10	US-09-799-462A-17	Seguence 17. Ann
	7	371.4	16.5	42999	11	US-09-836-911A-17	Sequence 17. Ann
	œ	371.4	16.5	42999	13	US-10-125-767-17	
	σ	371.4	16.5	42999	14	US-10-151-081-17	
	10	371.4	16.5	42999	14	US-10-287-313-17	1
	Ξ	371.4	16.5	42999	14	US-10-219-694-17	17
	12	368.2	16.3	1969	10	US-09-880-107-2231	2231
	13	360	16.0	427	11	US-09-918-995-19104	Sequence 19104.
ပ	14	352.2	15.6	416	11	US-09-918-995-5393	5393,
	12	349.8	15.5	393	11	US-09-918-995-36028	
O	16	333.4	14.8	343	10	US-09-796-692-8493	

Sequence 8493, Ap Sequence 2181, Ap Sequence 118, App Sequence 16, Appl Sequence 5, Appl	16, 7	Sequence 10, Apply Sequence 17863, A Sequence 2390, Ap Sequence 137, App Sequence 194, App Sequence 194, App Sequence 1642, A	28550 2408, 9042, 541,	Sequence 341, App Sequence 51, App Sequence 21, Appl Sequence 9, Appli Sequence 21, Appl Sequence 9, Appli
US-10-040-862-8493 US-10-106-698-2181 US-10-161-403-118 US-09-799-462A-16 US-09-815-981-5	US-09-836-911A-16 US-09-815-979-5 US-10-125-767-16 US-10-151-081-16 US-10-287-313-16 US-10-219-694-16 US-10-235-119-5 US-10-161-A03-18	10 10 10 10 10 10 10 10 10 10 10 10 10 1	-10-027-632-2 -09-867-701-2 -10-198-846-9 -09-878-178-5	10.446-502-5 -10-146-502-5 -09-815-981-9 -09-836-911A-
14 10 11 11	1111111111	101111	1040	2481111
343 536 17384 22118 22118	22118 22118 22118 22118 22118 22118	696 696 281 374 316 510	357 822 220	220 378 378 378 378
14.8 14.8 14.7 14.7	14.7 144.7 144.7 14.7 14.7	12.9 12.9 12.5 12.0 11.6	4.10 4.00 6.60	, თ თ თ თ თ ი თ თ თ თ თ
333.4 331.4 331.4 331.4	331.4 331.4 331.4 331.4 4.4 6.4 7.4 7.4 7.4	312.6 290.8 274.4 269.4	257.4 227.4 222.8 220	0000000 000000000000000000000000000000
c 17. 18 20 21	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	0 00 33 33 30 30 30 30	

## ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITE REPERENCE: PA005PI

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: US/02-03-29

PRIOR FILING DATE: 1099-09-29

PRIOR PLING DATE: 1099-09-29

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR PLING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1554.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (8)..(8)
LOCATION: (8)..(8)
NAME/KEY: misc_feature
LOCATION: (1553)..(1553)
OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-181/c; Sequence 181, Application US/10106698; Publication No. US20030109690A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%;
99.1%;
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 181
LENGTH: 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.15
Matches 1572; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-106-698-181
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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661 GAGTCCATCTTCCACCGCGGCCACGAGCG-CTTCCGCATTGCCAGCGCCTGCCTGGACGA

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	Db 526 CCTTCCTCCCCAGGCACCACTGGACCTTGAATTGCATTGGATCTC 467	1860 ACGCTGCCTCTGTGGTTCCCTCCTCTTTTCCTGGACGTGATAGCTCTGCCTATTGCA	OY 1920 GGACAATGATGGCTATTCTAAAGGCTAAGGAAAAAAACAAAC	QY 1980 ACTCAAGACTGACTTACAGACCAACCACCTTGCTGGAACCTTGCTAGCAGGCATT 2039	2040 CTTATAAAAGAAACTTTGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACT [	AGAGCOTCCTTACCTATGCTATGGATTTTTAATTTTTCTCTTATTTCATGTACACTG	2160 CTTTTTTGGTTACAGGATATCATGGAT 	OY 2220 ATTACAGTTTTTCAAAAAAA 2246 	RESULT 2 US-09-880-107-3600/c ; Sequence 3600, Application US/09880107	<pre></pre>	APPLICANT: Scherf, Uwe  APPLICANT: Gene Logic, Inc.  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  FILE REFERENCE: 44921-5028-WO	CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14	; PRIOR APPLICATION NUMBER: US bU/23/, US4 ; PRIOR ELLING DATE: 2000-10-02 ; NUMBER OF SEQ ID NOS: 3950 ; SOFTWARE: Patentin Ver. 2.1	; SEQ ID NO 3600 ; LENGHI: 432 ; TYPE: DNA ; ORGANISM: "Homo sapiens.	; FEATURE: ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 W79421 US-09-880-107-3600	Query Match 19.2%; Score 432; DB 10; Length 432; Best Local Similarity 100.0%; Pred. No. 4.1e-104; Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1816 GGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCACGCTGCCTCTGTGGT 1875	Oy 1876 TCCCTCCCTCATTTTCCTGGACGTGATAGCTCTGCCTATTGCAGGACAATGATGGCTAT 1935	Qy 1936 TCTAAACGCTAAGGAAAAAAAAAAACAAACAGAACTGTTTCAAGTACTCAAGACTGA 1995
$\cdot$	0 GCTGAGCTGCGAGTTCCTGCTGGCTGGGCCGGAGGGCCGGGGCGGGGGCGGGC	GCTGAGCTGCGGAGTTMCTGCTGGGGCCGGAGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGGGCCGGGG	SACCECATCRCCCCCACGGGGTCGGTGCCTGGGGGTCCTGTGCGATCCTGCAACAT   CACGGAGTCATACCCTGCTGTGCCCCCCATCTGGTCGTGGAGTCTGATGACCTTACTTT	O GGCTGCTTGGAGAGGCTGGTGGACATAAAGAAAGGAATACTGGTATGTGTGAGGACATACTTGCTATGTGTGTG	TCTGAAGAGGATCATCTCCGACCTGTGAAACTCTATAACTCCCTCAGGATCAGATGT	GGAGATGCTGGATCAACCCTTGCCAGCAGCAGCACACACA	AGATGAAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAAAGA 	GGAAGAGCCAGCTGAGGGCAAGAATCTGAAGATGATGGCATTGGAAAAGAAAACTTGGC 	CATCCTAGAGAAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTCTGG 	CTCGGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACAGAG	TTTCAAAGGCGGAAACTATGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGT 	CAAACTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGA	GAAAGAAGGAGCCGACTTCATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGA 	CCCACCATITGICAGGGITGICICCCAGICCICTCTGGAGGGIANGTICTGGGCGGAGG [	GGCCATCTGCATGGAACTTCTCACCAAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTC	AGTGATCATGCAGATCAGTGCCACACTGATGAAGGGAAAGCACGAGTGCAGTTGGAGC	CAACAAATCTCAATACAGTCTGACAAGAGCACAGGAGTCCTACAAGTCCTTGGTGCAGAT	CCACGAAAAAACGGCTGGTACACCCCCCAAAAGAAGACGGCTAACCCTGGGTATCAC	CCTTCCTCCCTCCCCAGGCACCACTGGACAATTACCTTTGAATGCTATTTGGATCTC  CCTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTC

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Sequence 8902, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION GRATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEC ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (1262)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (1263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1259)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (1260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n equals a,t,g,
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                                                 TTACCCACTCCCG 373
                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1269)
OTHER INFORMATION:
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NAME/KEY: SITE
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NAME/KEY: SITE
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OTHER INFORMATION:
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INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
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LOCATION: (1270)
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LOCATION: (1272
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LOCATION: (4089
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                                                                                                                                                                                                                                                                                                                               SEQ ID NO 8902
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                                              181 GGGCCGATCGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT 240
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NAME/KEY: misc_feature
LOCATION: 56, 57, 573, 614, 714, 750, 756, 770, 771, 784, 785, 807,
LOCATION: 819, 851, 859
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09919344
Patent No. US20020137911A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Yu, Jiangchun
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CAN
FILE REFERENCE: 210121.543
CURRENT APPLICATION NUMBER: US/09/919,344
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO14
LENGTH: 870
                                                                                                                                                                                                                                                                             TYPE: DNA.
ORGANISM: Homo sapiens
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US-09-764-891-10043/c
is Sequence 10043, Application US/09764891
; Publication No. US2003007780841
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILLE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10043
; LENGTH: 13076
                                                                                                                                                                                                                                     DB 11; Length 13076;
                                                                                                                                                                                                                                                                  1; Indels
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                           COTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE LOCATION: (5606)
COTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE COTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE COTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE COTHER INFORMATION: n equals a,t,g, or c US-09-764-891-8902
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
LOCATION: (1260)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
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   n equals a,t,g,
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OTHER INFORMATION:
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                 NAME/KEY: SITE
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Pred. No. 4e-87;
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (5606)
OTHER INFORMATION: n equals a,t,g,
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                                                                  LOCATION: (1263)
OTHER INFORMATION: n equals a,t,g,
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                           LOCATION: (1262)
OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 99.7%;
Matches 372; Conservative 0
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INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (4089)
OTHER INFORMATION: n equals
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INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
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LOCATION: (1270)
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LOCATION: (1311)
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Publication No. US20030033617A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                              3963 GGGCCGATCGCACCCCCCGTGGCGCGACGACCATTCGAACGTCTGCCCTATCAACT
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ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4350 La Jolla Village Drive, 6th Floor
      Pred. No. 8.5e-87;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION UNMER: 05/09/836,911A
FILING DATE: 17-Apr-2002
CLASSIFICATION: <UNKnown>
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FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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    99.78;
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      al Similarity 99.7
372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
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      Best Local
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                                                             3452 GGGCCGAICGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT 3393
                                          300
                                                                                                                    ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                    241 TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCGGGTGACGGGGAATCAGGGTTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/799,462A
FILING DATE: 10-Sep-2001
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/835,682
FILING DATE: 10.APR-1997
FILING DATE: 0.ABR-1996
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 12-UL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
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US-09-799-462A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09799462A Patent No. US20020160970A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
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MATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                               TTACCCACTCCCG 373
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TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND
                                                                                                                                                                                                                               Length 42999;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & MCAuliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
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Pred. No. 8.5e-87;
0; Mismatches 1
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACHENT TYPE: «Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
             INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 858-587-5360
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Best Local Similarity 99.7%;
Matches 372; Conservative
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STATE: CA
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Pred. No. 8.5e-87;
0; Mismatches 1;
                                                                                                                                                                                                                   NAME: Seldman, Stephanle L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NOV-2000
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 10-APR-1996
FILING DATE: 10-APR-1996
APPLICATION NUMBER: 08/629,825
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,825
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ANTI-SENSE: NO
FRAGMENT TYPE: <UNKNOWN>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10151081
Publication No. US20030083293A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.5%;
Best Local Similarity 99.7%;
Matches 372; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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US-10-151-081-17
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3963 GGGCCGATCGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT 4022
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                                                                                                                                                                                                                              APPLICANT: Hadlaczky, Gyula
APPLICANT: Hadlaczky, Aladar
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor
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REPLICATION NUMBER: 05/10/287,313
FILING DATE: 01-NO. US20030101480A1-2002
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/
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FILING DATE: 28 -NOV-2000
FILING DATE: 10-APR-1997
FILING DATE: 10-APR-1997
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/62,080
FILING DATE: 15-UUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-10-287-313-17; Sequence 17, Application US/10287313
Sequence 17, Application US/10287313; Publication No. US20030101480A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 858-450-8403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 858-587-5360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      4143 TTACCCACTCCCG 4155
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                                                                                                                                                                                                                                                                                                                                                                            361 TIACCCACTCCCG 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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                          ARTIFICIAL CHROMOSOMES, ÜSES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GGGCGATCGCACGCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
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                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 16.5%; Score 371.4; DB 1
Best Local Similarity 99.7%; Pred. No. 8.5e-87;
Matches 372; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: HEREWITH 05-WAR-2001
APPLICATION NUMBER: 09/724,693
FILING DATE: HEREWITH 28-NOV-2000
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/151,081
FILING DATE: 16-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-A0G-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-151-081-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/799,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
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TELEFAX: 858-587-5360
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MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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STRANDEDNESS: single
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKe
                                                                                                       SEQUENCES:
                                                                                                                                                                                                                                                         CITY: La Jolla
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Best Local Similarity
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                                                                                                                   GCTGACCCCCTTCGCGGGGGGATGCGTGCATTTATCAGATCAAGACCAACCCGGTCAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/10219694
Publication No. US20030108914A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                          9
                                                                                                                                                                                                                                     GGGCCGATCGCACGCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
                                                         1 CTCGCTCCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
                                                                                                                                 TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGA
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 DB 14; Length 42999;
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                              Indels
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ADDRESSEE: Heller Ehrman White & McAuliffe LLP STREET: 4350 La Jolla Village Drive, 7th Floor
Score 371.4; DB 1.
Pred. No. 8.5e-87;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/219,694
FILING DATE: 14-Aug-2002
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: <08/85,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/692,080
FILING DATE: 10-APR-1996
FILING DATE: 10-APR-1996
FILING DATE: 10-APR-1996
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESE Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
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16.5%;
ilarity 99.7%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: CA
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             Best Local Similarity
Matches 372; Conserv
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Score 371.4; DB 14; Length 42999;
Pred. No. 8.5e-87;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Useeph G.
APPLICANT: Scherf, Useeph G.
APPLICANT: Gene Logic, Inc.
TITLE G. INVENTION: Gene Expression Profiles in Liver Cancer; FILE REFERENCE: 44921-5028-W0.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR PPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2231, Application US/09880107 Patent No. US20020142981A1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
                                                                              INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
                                         858-587-5360
                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.5%;
Best Local Similarity 99.7%;
Matches 372; Conservative C
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                                                                <Unknown>
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                                                                                                                                                                                                                                             HYPOTHETICAL: NO
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                                              TELEFAX:
                                                                TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAAACTCAGCTGTGCTCCAGACTAGAGCCTCCTTACCTATGCTATGGATTTTAATTT
                                               160 GCTGGAACCCTTGCTAGCAGGCATTCTTATAAAAGAAACTTTCGAGCCTCCTTATATATGC
                                                                                                                      220 TGGAAACTCAGCTGTGCTCCAGACTAGAGCCTCCTTACCTATGCTATGGATTTTTAATTT
                                                                                                                                                      GCTGACCCCCTTCGCGGGGGGGATGCGTGCATTTATCAGATCAAGACCAACCCGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCGATCGCACGCCCCCCGTGGCGGCGACGACCCATTCGAACGTCTGCCCTATCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 TTATATGTAGTCACCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 352.2; DB 11;
Pred. No. 5.6e-83;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILLE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5393
                                                                                                                                                                                                                                                                                                                              Sequence 5393, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
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; OTHER INFORMATION: n = A,T,C or
US-09-918-995-5393
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Best Local Similarity 97.5%;
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-918-995-5393/c
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                                                                                                                                                                       Gaps
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0
                     FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 M10098
NAME/KEY: unsure
LOCATION: (1)..(1969)
OTHER INFORMATION: n = a or c or g or t
                                                                                                                                   DB 10; Length 1969;
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Publication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                   Indels
                                                                                                                      Score 368.2; DB 10;
Pred. No. 8.5e-87;
----hes 3;
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Pred. No. 4.9e-85;
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100.0%; Pred. No. ...
'... 0; Mismatches
                                                                                                                                                                  0; Mismatches
                                                                                                                                 Query Match 16.3%;
Best Local Similarity 99.2%;
Matches 370; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITACCCACTCCCG 600
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US-09-918-995-19104
         ORGANISM: Homo sapiens
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1722 CAAGTCCTTGGTGCAGATCCACGAAAAAACGGCTGGTACACACCCCCAAAAGAAGAAGG 1781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1842 ATGCTGTATTTGGATCTCACGCTGCCTCTGTGGTTCCCTCCTCATTTTTCCTGGACGTG 1901
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                                                                                                               Sequence 36028, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 2011-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT PILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01.20
; PRIOR FILING DATE: 1999-01.20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FESESCE for Windows Version 3.0
; SEQ ID NO 36028
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Pred. No. 2.3e-82;
0; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.5%;
93.1%;
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Best Local Similarity 93.1
Matches 366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36028
JS-09-918-995-36028
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Search completed: August 4, 2003, 21:38:08 Job time : 655 secs

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BX404169 BX404169
BX32452 AL57525
BX324562 BX334562
AL535478 AL535478
BM452095 AGENCOURT
CD107494 AGENCOURT
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AL526276 AL526276
AL526276 AL526276
AL556878 AL556878
BU509450 AGENCOURT
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BU508125 AL573125
BW803766 AGENCOURT
AF116721 HOMO SAPI
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BU51712 AGENCOURT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Titoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                        AL526276
AL541381
AL548646
AL56878
BU509450
BX419858
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BQ228412
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BU515543
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BU166850
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BM715207
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HTC; CAP trapper.
Mus musculus (house mouse)
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Copyright (c) 1993 - 2003 Compugen Ltd
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Arakawa,T., Hara,A., Fukunishi,Y., Ronno,H., Adachi,J., Fukuda,S.,
Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischman,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Baldarelli,R., Barsh,G., Blake,J., Bofielli,D., Bojunga,N.,
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Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Marchlonni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conns.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conns.

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Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., SasaKi,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Barada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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Yonda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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RIKEN integrated sequence analysis (RISA) system--384-format
Genome Res. 10 (11), 1757-1771 (2000)
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/note="unnamed protein product; NICE-5 PROTEIN (PRO3094)
homolog [Homo sapiens] (SPTR|09UGL6, evidence: FASTY,
100%ID, 100%length, match=213)
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/db_xref="MGI:1902377"
/db_xref="taxon:10090"
/clone="2310012M18"
/sex="male"
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94.3%; Pred. No. 1.6e
tive 0; Mismatches
                                                                                                                                                                                                                            1. .1408
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                       Location/Qualiflers
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Best Local Similarity 94.3
Matches 1333; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 1201)  AUTHORS 11, W. B., Gruber, C., Jessee, J. and Polayes, D.  TITLE Unpublished  COMMENT CONTACT: Genoscope  CONTACT: Genoscope  CONTACT: Genoscope - Centre National de Sequencage  BP 191 91006 EVRY cedex - France  BP 191 91006 EVRY cedex - France  Email: sequefégenoscope.ons.fr, Web: www.genoscope.cns.fr  Library was constructed by Life Technologies, a division of  Invitrogen. This sequence belongs to sequence cluster 78.r For more  information about this cluster, see http://www.genoscope.cns.fr  CG1-bin/Cluster.cg12seq-CSODE004BE02NP16cluster=78.r. Contact:	Feng Liang Wall Liangellitetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODE004BE02NP1. Location/Qualiflers Location/Qualiflers 11201 /mol.type="mRNA" /mol.type="mRNA" /mol.type="mRNA" /tissue_type="ptacENTA" /tissue_type="ptacENTA" /clone="CSODE0044104" /tissue_type="ptacENTA" /clone="CSODE0044104" /tissue_type="ptacENTA" /clone="CSODE0044104" /tissue_type="ptacENTA" /clone="CSODE0044104" /tissue_type="ptacENTA" /clone="CSODE0044104" /tissue_type="ptacENTA" /clone="csode047"	DASE COUNT 283 a 244 c 270 g 356 t 48 others  ONEGIN  ONETY MATCh 48.1%; Score 1083.2; DB 9; Length 1201;  Bast Local Similarity 97.0%; Pred. No. 2.6e-161;  Matches 1102; Conservative 18; Mismatches 14; Indels 2; Gaps 2;	OY 1075 TCAGAAGATGAAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATG 1134	Qy         1195         TTGGCCATCCTAGAGAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTG         1254           Db         1019         TTGGCCATCCTAGAGAAAATTAAAAAGAACCAGAGGCAAGATWACTTAAATGGTGCAGTG         960           Qy         1255         TCTGGCTGGTGCAGGCCACTGACGGCTGATGAAGGAGCTCAGGGATATATACCGATCA         1314           Db         959         TCTGGCTCGGTGCAGGCCACTGACGGCTGATGAAGAGGAGCTCAGGGATATATACCGATCA         900	QY         1315 CAGAGTTTCAAAGGCGGAAACTATGCAGTCGAACTCGTGAATGACTGTATGATTGG           1315 CAGAGTTTCAAAGGCGGAAACTATGCAGTCGTGAATGACAGTCTGTATGATTGG           1317 CAGAGTTTCAAAGGCGGAAACTATGCAGTCGTAATGACAGTCTGTATGATTGG           1318 CAGAGTTTCAAAGTTGACCAGGACAGCGCTTTGCACAAGGATCTCCAGATCCTC           1319 CAGAGTCAAAGTTGACCAGGACAGCGCTTTGCACAAGGATCTCCAGATCCTC           1319 CAGAGTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCTCTC           1310 CAGAGTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCTC	QY         1435 AAAGAGAAGGAGCCGACTTCATTCTACTTAACTTTCCTTTAAAGATAACTTTCC         1494           T79 AAAGAGAAAGAAGGAGCCGACTTCATTCTAACTTTCCTTTTAAAGATAACTTTCC         720           QY         1495 TTTGACCCACCATTGTCAGGGTTGTGTCTCCAGTCCTCTGGAGGTATGTTCTGGC         1554           Db         719 TTGACCCACCATTGTCAGGGTTGTGTCTCCCAGTCCTCTGGAGGTATGTTCTGGC         160           QY         1455 TTTGACCCACCATTGTCAGGGTTGTTCTCCAGTCCTCTGGAGGTATGTTCTGGC         160           QY         1555 GGAGGGCCATTGCATGGAACTTCTCCCAAACAGGGTTGTCTCCCATA         1614           Db         659 GGAGGGCCATCTGCATGGAACTTCTCCCAAACAGGGCTGGAGCTATCCCATA         600
03   03   04   05   05   05   05   05   05   05	Db   725   GAGGTGCCATCTCCCAAGCCAGGCTGGAGGCTGCTTTTTTTT	QY         1796         TCACCCTCCTCCCTCCCCCAGGCACTGGACCAATTACCTTTGAATGGTGTATTGGA         1855           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         1916 TGCAGGACAATGATGGTATTCTAAACGCTAAGGAAAAAAAA	OY 2026 TGCTAGCAGGCATTCTTATAAAAGAAACTTTCGAGCCTCCTTATATGCTGGAAACTCAG 2085	QY         2146 TTTCATGTACACTGCTTTTTTGGTTACAGTGTATGATGGATG	RESULT 2 AL540967/C LOCUS LOCUS AL540967 LOCUS AL540967 LOCUS DEFINITION AL540967 ACCESSION AL540967 ACCESSION AL540967 ACCESSION AL540967 AST CONTINUE CONTINU

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 GAGTCAGTGATCATGCAGATCAGTGCCACACTGGTGAAGGGGAAAGCACGAGTGCAGTTT 1674
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                                                     ATCTCACGCTGCCTCTGGGTTCCCTCCTCATTTTCCTGGACGTGATAGCTCTGCCTA
                                                                                                                                                                                              ATCTCACGCTGCCTCTGTGGTTCCCTCCTCATTTTTCCTGGACGTGATAGCTCTGCCTA
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CDNA Library Arrayed by: The I.M. A.G.E. CONSORTHUM (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
flound through the I.M.A.G.E. Consorthum/LLNL at:
http://mage.lnl.gov
Plate: LLAM14057 row: 1 column: 01
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National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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/mol_type="mRNA"
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Location/Qualifiers
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VERSION
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TITLE
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/db_xref="taxon:9606"
/clone="IMAGE:6502128"
//tlssue_type="lelomyosarcoma"
/lab_host="DHDB (phage=resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; cloned unidirectionally. Primer: Oligo dT. Average liner: is 12 2 1 kb. " 3 others
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                                                                                                                                                                                     Length
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Pred. No. 2.3e-152;
0; Mismatches 26; Indels
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ilarity 97.5%;
Conservative
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188 CCCGCCGGCCCCGGAGGAACGCGNAGGATGCAGCAGCCGCAGCGGGGCAGC 247	545 AGCAGCCGGGGCCGGGCCAGCAGCTGGGGGCCCAGGGGCGCCCGGGGGCCGGGGGCG 60	605 GCCCAGGGGGGCCCGGGGCCCGGGCCTGAGGCGAGAGCTGAAGCTGCTCGAGT 664	665 CCATCTTCCACGGGCCACGAGGGCTTCCGCATTGCCAGGGGCTGGCT	725 -GCTGCGAGTTCCTGCTGGCGCCGGAGGGCCCGGGGGGGGG	785 AICTCCCCCCAGGGGGTCGGTGCCTGGGGATCCTGTCCGCTCCACTGCAACATCAGG 844	845 AGTCATACCCTGCTGTGCCCCCATCTGGTCGGAGTCTGATGACCCTAACTTGGCTG 904	905 CTGTCTTGGAGGGCTGGTGGACATAAGAAAGGGAATACTCTGCTGTTGCAGCATCTGA	965 AGAGGATCATCTCCGACCTGTGTAAACTCTATAACCTCCCTC	1025 TGCTGGATCAACCCTTGCCAGCAGAGCACACAGGAAGACGTGTCTTCAGAAGATG 1084 11111111111111111111111111111111111	1085 AAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAAAGAGGAAG 1144 	1145 AGCCAGCTGAGGCAAGAAATCTGAAGATGATGGCATTGGAAAAGAAACTTGGCCATCC 1204 	1205 TAGAGAAAATTAAAAGAACCAGGGAAGATTACTTAAATGGTGCACTGTCTGGCTCGG 1264 	1265 TGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGTTTCA 1324	1325 AAGGCGGAAACTATGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGTCAAAC 1384 	1385 TCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGAGAAAG 1444 	1445 AAGGAGCCGACTTCATTCTACTTAAACTTTTCCTTTAAAGATAACTTTCCCTT 1496 	RESULT 5 AL565939/C LOCUS LOCUS DEFINITION AL565939 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF0009108 3-PRIME, mRNA sequence.
qa	QY Up	QV	Qy Db	Qy	Qy .	QY	Qy Db	Qy	Qy	Qy	Qy Db	Qy Db	Qy	Qy Db	Oy Db	QQ QD	RESI AL50 LOCI DEF
851 CCTCTGTGGTTCCCTCCTTTTTCCTGGACGTGATAGCTCTGCCTATTGCANNGACA 910	CTCAA 1	1986 GACTGACTTACAGACCAACCACCTTGCTGGAACCTTGCTAGCAGGGTTCTTATA 2045 	2046 AAAGAAACTTTCGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACTAGAGC 2104 		DECUSION ALS40968 Home sapiens PLACENTA Home sapiens CSODE004XIO4  DEFINITION ALS40968 Home sapiens PLACENTA Home sapiens cDNA clone CSODE004XIO4  S-PRIME, MRNA sequence.  ACCESSION ALS40968 GENERAL SEGUENCE.	S EST. Homo sapiens (human)	ENKATYOTE, Metazoa; Chordata; Crandata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS 1 (bases 1 to 1201) AUTHORS 11, W.B., Gruber; C., Jessee, J. and Polayes, D.	ΑΓ		Sub	FATURES Location/Qualifiers sequence ID : CSODE004BE02QP1. FATURES Location/Qualifiers source I. : 1201 //rranism=Homo sarians"	/mol_type="mRNA" /db_xref="taxon:9606" /clone="CSD004"  /fiseighth:		the Not I and Ecory sites of the pCMVSPORT 6 vector.  Library was not normalized." 24 others  ORIGIN 273 a 303 c 400 g 201 t 24 others	Ouery Match  Ouery Match  Best Local Similarity 95.8%; Pred. No. 3.7e-152;  Matches 1084; Conservative 18; Mismatches 23; Indels 7: Gans 5:	.ACTCCCGGAGGTGGCGGCGCGCCATCTTGGCCAAGGGGGGGATCAGGAAGTGCGGACC 42	425 GCGGCGGCGGCGGCGGCGGCGGCGGGGGCCGGAGGCCCGAGGCCCGGAGGCTCCCGG 484

1846

1906

380

1726

500

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRI cedex - France
Bmail: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Enail: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 78.r For more
information about this cluster, see http://www.genoscope.cns.fr/
cigi-bin/cluster.cgi7seq-CLOBB0178HINRDiscluster=78.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2146 TITCAIGTACACTGCTITITIGGITACAGTGTATGATGGATGTGTATGAAAAAATGTA 2205
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     TGCAGTTTGGAGCCAACAAATCTCAATACAGTCTGACAAGAGCACAGAGCAGTCCTACAAGT
                                                                                                                     679 TICTGGGCGGAGGGCCATCTGCATGGAACTTCTCACCAAACAGGGCTGGAGCAGTGCCT
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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19 KGTTTGGGAAGRGAATTA 2
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B
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 78:r For more
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF009BE04NPl&cluster=78:r. Contact:
Feng Liang Email: fliang@llfetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF009BE04NPl.
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/note="Organ: Drain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
                                                                        Euteleostomi;
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                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases I to 1182)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full:Length cDNA libraries and normalization
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280 c 192 g 341 t 77 others
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88.5%; Pred. No. 1.4e-139;
iive 59; Mismatches 63;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/dev_stage="fetal"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CS0DF009Y108"
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     GI:30550439
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/organism="Nomo sapiens"
//organism="Romo sapiens"
//organism="Romo sapiens"
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//clone="CSODIO87YE04"
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//clone=lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
//orde="1st strand CDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCNVSPORT 6 vector. Library was normalized."
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                                                           CTGGCTCGGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCAC 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Lintitrogen. This sequence belongs to sequence cluster 78 r. For mc
information about this cluster, see http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIO87DA02NP1&cluster=78.r. Contact:
http://wlllength.invitrogen.com/ InvitroGen.Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO87DA02NP1.
                                                                                                                                                                                                    TGGCCATCCTAGAGAAATTAAAAAGAACCAGAGGCAAGATTACTTAAAATGGTGCAGTGT
                                                                                                                                                                                    ATGTCAAACTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-tength cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the CENVSPORT 6 vector. Library was normalized.

185 c 229 g 255 t 11 others Chordata; Craniata; Vertebrata; Euteleostoml; Primates; Catarrhini; Hominidae; Homo. Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequeféquencope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 78 r For mc
Information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOAQCO25AA10NP16.cluster=78 r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fullength.liviltrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOACQC25AA10NP1. AACCCTGGAGTATCACCCTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTTGAAT GAGTGCAGTTTGGAGCCAACAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACA AGTCCTTGGTGCAGATCCACGAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGCT TCCAGATCCTCAAAGAGAAAGAAGGAGCCGACTTCATTCTACTTAAACTTTTCCTTTAAAG ATAACTTTCCCTTTGACCCACCATTTGTCAGGGTTGTGTCTCCAGTCCTCTTGGAGGGT ATGTTCTGGGCGGAGGGGCCATCTGCATGGAACTTCTCACCAAACAGGGCTGGAGCAGTG 1304 TATACCGATCACAGAGTTTCAAAGGCGGAAACTATGCAGTCGAACTCGTGAATGACAGTC ö DB 13; Length 919; Indels Eukaryota, Metazoa; Chordata; Craniata; Verte Mammalla; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 919) LI, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization 40.4%; Score 911.4; DB 13 98.8%; Pred. No. 3.7e-134; ive 10; Mismatches 1; /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" Query Match 40.4% Best Local Similarity 98.8% Matches 906; Conservative Contact: Genoscope 1.919Unpublished 739 1424 799 1484 1544 619 1604 1664 1724 619 559 499 BASE COUNT ORIGIN REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES g á a òγ

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/mol_type="mRNA"
/do_type="mRNA"
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74 a 266 c 376 g 218 t 47 others
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Confact: Genoscope Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 FVRY cedex - France
Bmall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of information about this sequence belongs to sequence cluster 78 r For information about this cluster, see http://www.genoscope.cns.fr/cgl-bin/cluster.ggl?seq=CSODF09BE04QP16cluster=78 r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF009BE04QP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Score 899.8; DB 9;
Pred. No. 2.3e-132;
                     24; Mismatches
 39.9%;
90.5%;
                       Conservative
Query Match
Best Local Similarity
Matches 997; Conserv
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BX378721 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
COLOne CSODIO24YM15 5-PRIME, mRNA sequence.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
241 CGGAAACTATGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGTCAAACTCT
                                                               AGCCGACTTCATTCTAACTTTTCCTTTAAAGATAACTTTCCCTTTGACCCACCATT
                                                                                                                             TGTCAGGGTTGTGTCTCCAGTCCTCTGGAGGGTATGTTCTGGGCGGAGGGGCCATCTG
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                                                CAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGAAGAAGA
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BP 191 91006 EVRY cedex - France
Emall: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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E I (bases 1 to 1070)

S NIH-MGC http://mgc.nd.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ArCC/DCTP/PTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

High quality sequence stop: 653.

Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:5526427
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   GATCCTCAAAGAGAAGAAGGAGCCGACTTCATTCTACTTAACTTTTCCTTTAAAGATAA 1487
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llarity 96.9%; Pred. No. 2.4e-131;
Conservative 0; Mismatches 26;
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                                                                 1488 CTTTCCCTTTGACCCACCATT 1509
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AGENCOURT_6386309 NIH_MGC_72
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                                                                                                                                                                                                              5', mRNA sequence.
BM452095
BM452095.1 GI:18501135
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/mol_type="mRNN"
/db_xref="taxon:9606"
/clone="IMAGE:30365487"
/tissue_type="Pituitary"
/tab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NHH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: NotI: Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
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                     GGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGTTT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                         CCTAGAGAAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTCTGGCTC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can leound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
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Pred. No. 6.8e-127;
0; Mismatches 11;
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    .895
    /organism="Homo sapiens"

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98.7%;
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                                                                                                                             // Organism="Homo sapiens"
// Organism="Homo sapiens"
// Ab_Lxref="taxon:9606"
// Ab_Lxref="taxon:9606"
// Clone="CSODIOJAMIS"
// Lissue_type="FLACEWIA COT 25-NORMALIZED"
// Clone_lib="Homo sapiens PLACEWIA COT 25-NORMALIZED"
// Orde="1st strand cDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized."
58 a 277 c 357 g 184 t 19 others
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Invitrogen. This sequence belongs to sequence cluster 78.r For mc information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi/Seq-CSOD1024AG08QP16cluster=78.r. Contact; Feng Liang Email : filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOD1024AG08QP1.
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15; Mismatches 39;
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Best Local Similarity 93.9%;
Matches 978; Conservative 15
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_txef="taxon:9604627"
/clone="IMAGE:6044627"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_line="NHLMGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library."
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                         (MGC)
                                                         Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://inage.llnl.gov
Plate: LLAM13287 row: i column: 12
High quality sequence stop: 724.

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8
          NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Unpublished
Contact: Robert Strausberg, Ph.D.
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Pred. No. 4.2e-123;
0; Mismatches 8;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Contact the Not 
                                                  1201 bp mRNA linear EST 12-MAY-2003
Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006YB05
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 78.r For mc
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/Cluster.cgi?seq-CSDE0066CA03QPl&cluster=78.r. Contact:
Feng Liang Email: fliang@lifete.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE006CA03QPl.
Location/Qualifiers
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On Feb 15, 2001 this sequence version replaced g1:12872399.
Contact: Genoscope
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Pred. No. 5.8e-123;
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92.1%; Pred. No. 5...
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287 c 366 g 224 t
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/clone="CS0DE006YB05"
                                                                                                                                        AL541381.2 GI:30545506
                                                                                        5-PRIME, mRNA sequence.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein

(without alignments)
807.019 Million cell updates/sec July 29, 2003, 13:35:23 ; Search time 83 Seconds Run on:

US-10-005-549-2 2229 1 MQPQPQGQQQQPGPGQQLGG......KSLVQIHEKNGWYTPPKEDG 422 Title: Perfect score: Sequence:

1107863 seqs, 158726573 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
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## SUMMARIES

Description	Human RATLId6 (red	Human colon cancer	Human prostate can	Novel human protei	Human RATLId6 tran	Human ORFX ORF1537	HTRM clone 3340290	Drosophila melanog	Human RATL1d6 ubiq
а	AAE24493	AAG73684	AAY48312	ABB97360	AAE24494	AAB41773	AAY73387	ABB59516	AAE24524
<b>8</b>	23	22	20	23	23	21	21	22	23
% Query Match Length DB I	422	374	291	340	245	263	308	397	164
% Ouery Match	100.0	83.6	67.7	58.3	58.0	56.8	50.3	45.8	37.4
Score	2229	1863	1509	1300.5	1293	1266	1120.5	1020.5	834
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Drosophila melanog	ď		⊏	human	human	human	human	liver	н	Human brain expres	Human bone marrow	Peptide #7087 enco	Human peptide enco	Yeast Cdc34 protei	=	Novel human diagno	Aspergillus fumiga		Candida albicans e	Drosophila melanog	Human ovarian anti		Human UBE2 related	. Human polypeptide	Human tumour marke	Human ORFX ORF843	FLJ10378 fis clone	Human intracellula	Clam cyclin-select	Arabidopsis thalia	Drosophila melanog	Novel human diagno	B. burgdorferi 79	•	C glutamicum prote
ABB67021	ABB60719	ABB60722	ABG11969	ABG28233	ABG15534	ABG20796	ABG03538	ABG54524	ABB39508	AAM60200	AAM72820	AAM33050	ABG42649	AAE28245	ABB63741	ABG03535	ABJ26294	ABJ25694	ABP73432	ABB63097	ABP41187	AAB43031	ABP71416	AAO02768	ABB77435	AAB41079	ABP43569	ABJ19401	AAW31278	AAG42118	ABB59024	ABG20670	AAR30730	ABB54116	AAG91922
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### ALIGNMENTS

AAE24493 standard; Protein; 422 AA. 04-OCT-2002 (first entry) AAE24493; 

RESULT

Human RATL1d6 (regulated in activated T-lymphocyte 1d6) protein.

Human; ublguitin conjugating enzyme; UBC; RATLId6; immune disorder; regulated in activated T-lymphocyte 1d6; neuronal disorder; cancer; tumour; lymphoproliferative; cancer; democarcinoma; heukaemia myeloma; sarcoma; neurodegenerative; Inflammatory; rheumatoid arthritis; asthma; multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia; depression; epilepsy; acquired immuno deficiency syndrome; altergy; MIDS; anaemia; atopic dermattis; diabetes mellitus; dermatological; myocardial infarction; renal tubular acidosis; gonadal dysgenesis; anticonvulsant; ortostatic; neuroprotective; nootropic; anti-HIV; ophthalmological.

Homo sapiens.

Location/Qualifiers 89..333 /note= "Transmembrane domain" Key Domain

WO200236741-A2

10-MAY-2002.

```
The invention relates to a novel ubiquitin conjugating enzyme (UBC)
homologue, RATL1d6 (regulated in activated T-lymphocytes 1d6) and its
corresponding nucleic acid. The invention also relates to methods for
treating, diagnosing, preventing and screening for disorders related
to the expression of RATL1d6. UBC is useful for screening for candidate
compounds capable of binding to and/or modulating its activity. UBC is
useful for treating an immune or neuronal disorder in a mammal. The
method is useful for treating a cancer or tumour. It is useful for
suppressing the immune response in a subject requiring the suppression.
It is also useful for treating lymphoproliferative disorder, cancer e.g.
adenocarcinoma, leukaemia, myeloma, sarcoma, etc, neurodegenerative
disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma,
multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's
disease, dementia, depression, epilepsy, etc, immune disorder or immune
related disorders such as acquired immuno deficiency syndrome (AIDS),
allery, anaemaia, atopic dermatitis, disbetes mellitus, myocardial
tubular acidosis, gonadal dysgenesis, dysplasia, cataract, etc. The
present sequence is human RATL1d6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2229; DB 23; Length 422; 100.0%; Pred. No. 7.7e-181; ive 0; Mismatches 0; Indels 0;
                                                                                                                        W, Finger JN;
                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                 Claim 6; Fig 3; 169pp; English.
                                30-OCT-2000; 2000US-244688P. 30-JUL-2001; 2001US-308706P.
29-OCT-2001; 2001WO-US46559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 422; Conservative
                                                                                                                      Bowen MA, Wu Y, Yang
                                                                                                                                                       WPI; 2002-479758/51.
N-PSDB; AAD39359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 AA;
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cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon. Cancer antigens have cytostatic activity and cancer antigens. The colon. Cancer antigens have cytostatic activity and cancer antigens. The colon. Cancer antigens have cytostatic activity and cancer in appropriate production. N and P may be used in the prevention, chargesion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing the nucleic acids into a host cell and culturing the cell of the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell of the cancers. Ashaying the cell and treatment of colorectal carcinomas and cancers. Ashaying to Ashaying represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 FRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCNITESYPAVPPI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 WSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPLPAE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 FRIASACLDELSCEXLLAGAGGAGAAPGTASPPTGSVPGDPVRIHCNITESYPAVPPI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 1863; DB 22;
Pred. No. 8.6e-150;
0; Mismatches 6:
                                                                                                                                                                                                                                                  Human colon cancer antigen protein SEQ ID NO:4448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 6262-6264; 9803pp; English.
                                                                                                                                 AAG73684 standard; Protein; 374 AA.
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98.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                            (first entry)
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Best Local Similarity 98.4°
Matches 358; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                           colorectal carcinoma
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WO200122920-A2.
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                                                                                                                                                                                                          03-SEP-2001
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                                                                                                                                                                       AAG73684;
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The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
expressed sequence tag.
                                                                                                           LERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDED
                                                                                                                                                                                               EEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQ
                                                                                                                                                                                                                                                                                                                ADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIM
                                                                                                                                                                                                                                                  ATDRIMKELRDIYRSQSFKGGNYAVELVND$LYDWNVKLLKVDQDSALHNDLQILKEKEG
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis \cdot
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                                         Length 291;
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                                       Score 1509; DB 20;
Pred. No. 7.6e-120,
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Wehrman T, Drmanac RT;
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 628; 509pp; English.
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                                           6/...
100.08; P.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001; 2001WO-US26015.
                                       67.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                         Conservative
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                                                         Similarity
       291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYSE-) HYSEQ INC.
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Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABN32546
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                                                                         291;
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        Sequence
                                         Query Match
                                                           Local
                                                                         Matches
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                                                                       190
                                                                                                  11 GWSSAXSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIHEKNGWYTPP 370
WSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPLPAE 130
                                                                                                                                                                      LHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQ 358
                                                                                                                                                                                                                                              418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used. (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. ANY48304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenthal A;
                                                    GWSSAYSIESVIMOISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQIHEKNGWYTPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate cancer-associated protein 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY48312 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; 128; 194pp; German.
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N-PSDB; AAZ33482.
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 71
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                                                                                                                                                                                  DPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKL 159
                                                                                                                                                                                                                                                                                                                                                                                                          VLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulated in activated T-lymphocyte 1d6; neuronal disorder; cancer; tumour; lymphoproliferative; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; neurodegenerative; inflammatory; rheumatoid arthritis; asthma; multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia; depression; epilepsy; acquired immuno deficiency syndrome; allergy; ALDS; anaemia; atopic dermatitis; diabetes mellitus; dermatological; myocardial infarction; renal tubular acidosis; gonadal dysgenesis; dysplasia; cataract; cytostafic; neuroprotective; nootropic; anti-HIV; anticonvulsant; antiinflammatory; Cushing's syndrome; cardiant;
                                                                                                                             66
                                                                                                                                                        51
                                                                                                                                                                                                               94
e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                          LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPH-LPPRGSVPG
                                                                                                                                          160 YNLPQHPDVEMLDQPLPAEQCTQEDVSS--EDEDEEMPEDTEDLDHYEMKEEEPAEGKKS
                                                                                                                                                                                                                                                                                              EDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVE
                                                                                                                                                                                                                                                                                                                                                    LVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSP
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ubiquitin conjugating enzyme; UBC; RATL1d6; immune disorder;
                                                                    Length 340;
                                                                                                 53;
                                                                                                                                                                                                  Indels
                                                                      DB 23;
                                                                    58.3%; Score 1300.5; DB 23, 67.8%; Pred. No. 5.1e-102; ive 30; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQOSYNSIVQIHEKNGWYTPPKEDG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQQSYKSLVQIHEKNGWYTPPKEDG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RATL1d6 transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE24494 standard; Protein; 245 AA
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30-JUL-2001; 2001US-308706P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                 al Similarity 67.8
261; Conservative
                                        340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ophthalmological;
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                                                                    Query Match
Best Local S
Matches 261
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The invention relates to a novel ubiquitin conjugating enzyme (UBC) homologue, RATLIG6 (regulated in activated T-lymphocytes 1d6) and its corresponding nucleic acid. The invention also relates to methods for treating, diagnosing, preventing and screening for disorders related to the expression of RATLIG6. UBC is useful for screening for candidate compounds capable of binding to and/or modulating its activity. UBC is useful for treating an immune or neuronal disorder in amammal. The method is useful for treating a cancer or tumour. It is useful for suppressing the immune response in a subject requiring the suppression. It is also useful for treating lymphoproliferative disorder, cancer e.g. adenocarcinoma, leukaemia, myeloma, sarcoma, etc., neurodegenerative disorder, inflammatory disorders e.g. rheumatcid arthritis, asthma, multiple sclerosis, psoriasis, etc., neuronal disorders e.g. Alzheimer's disease, dementia, depression, epilepsy, etc. immune disorder or immune companies and acquired immuno deficiency syndrome (AIDS), and acquired immuno deficiency and acquired immuno deficiency and acquired immuno deficiency and acquired immuno deficiency and acquired a
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                                                                                                   Novel ubiquitin conjugating enzyme polypeptide isolated from activated numan T cell, for screening modulators useful for treating cancer, immune disorder, lymphoproliferative disorder, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 LKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKE
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100.0%; Pred. No. 1.4e-101;
ive 0; Mismatches 0;
Finger JN;
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Best Local Similarity 100.0
Matches 245; Conservative
Wu Y, Yang
                                                  WPI; 2002-479758/51.
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  Bowen MA,
                                                                                                                                                                                                                                 Claim 6;
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX control of the protein of the protective; shelpertities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; cathibsorian; cordana; thrombolytic; immunosuppressant; municostimulant; cardana; thrombolytic; coaquiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive; antidatamenty; and antidanaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating to pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy. Conclete acids can be used to express ORFX proteins in gene therapy. Conclete acids can be used to express ORFX proteins in gene therapy. Conclete acids and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, concliterative disorders, cardiovascular disease, diabetes mellitus, cholesterol ester storage, systemic lupus confirmed immunodeficiency (SCID), AIDS, viral, confirming the infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coaquiation; to inhibit thrombosis; and as a contraceptive. <u>8</u> antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antilnflammatory disease; coaqulation; PCLRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVP Gaps × Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease antirheumatic; antithyroid; .; ' 56.8%; Score 1266; DB 21; Length 263; 94.3%; Pred. No. 3e-99; Indels 6 Pred. No. 3e-9 4; Mismatches antibacterial; antifungal; Claim 11; Page 2294; 5507pp; English. 31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763. 31-MAR-2000, 2000WO-US08621 thrombosis; contraceptive. Query Match 56.8 Best Local Similarity 94.3 Matches 246; Conservative Leach M; (CURA-) CURAGEN CORP. WPI; 2000-602362/57 263 AA; N-PSDB; AAC75982 WO200058473-A2. Shimkets RA, Homo sapiens. 05-0CT-2000 33 Sequence

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AAY73325-Y73389 are human transcriptional regulator molecule (HTRM)

protein sequences. The HTRM protein and nucleotide sequences are useful

for preventing or treating disorders associated with decreased expression

or activity of HTRM which include cell proliferative disorders such as

carteriosclerosis and cirrhosis; cancers including adenocarcinoma and

leukaemia; immune disorders such as AIDS, Addison's disease, diabetes

carteriosciated arthritis, multiple sclerosis, systemic lupus

cerythematosus, and myasthenia gravis; infections and trauma. Antagonists

of the HTRM polypeptides are useful for treating or preventing disorders

cof the HTRM polypeptides are useful for treating or preventing disorders

cof the HTRM polypeptides are useful for treating or preventing concernation in the properties of compounds in drug screening techniques.

Cof screening libraries of compounds in drug screening techniques.

Cof mRNA and regulating gene function by modulating the activity of frammatorial compounds and the activity of fractions and the activity of fraction by modulating the activity of fractions and specifically bind HTRM and polypucleds encoding HTRM or agonists can also be used to prevent concernation and the HTRM and pregulating the decreased HTRM expression. Antibodies
276
                                                                                  for diagnosing disorders associated with the expression of HTRM, particularly in assays that detect the expression of HTRM. Nucleotide sequences encoding HTRM may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; Addison's disease; multiple sclerosis; rheumatod arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treament.
                                                           219 DDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRD-IYRSQSFKGGNY-AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides useful for diagnosis, prevention and treatment of cancer and immune disorders
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    Reddy F
Azimzai F

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Patterson C, Baughn MR,
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                                                                                                                                                                                                                                                                                                                                                                                                               HTRM clone 3340290 protein sequence.
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                                                                                                                                                                                                                                                                                        AAY73387 standard; Protein; 308 AA
                                                                                                                                            277 ELVNDSLYDWNVKLLKVDQDS 297
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98US-0095827.
98US-0102745.
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Gerstin EH,
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62 GDPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCK 121 GDPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCK 158

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159 LYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSE 218

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Interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
differences in gene sequences among normal, carrier and affected individuals. Using diagnostic assays, cancer can be detected prior to the appearance of clinical symptoms and thereby progression of cancer be prevented by aggressive treatment or preventive measures.
                                                                                                                                                                                                             160 YNLPQHPDVEMLDQPLPAEQCTQEDVSS--EDEDEEMPEDTEDLDHYEMKEEEPAEGKKS
                                                                                                                                                                               EDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVE
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                     DB 21; Length 308
                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 5340
                                                    50.3%; Score 1120.5; DE 59.7%; Pred. No. 9e-87; iive 29; Mismatches 4
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11-JUL-2000; 2000US-0614150
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                                                             Similarity
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                                      308 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01876-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 ILLINFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 PVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEEEPAEGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATLVKGKARVQFGANKS----QYSLTRAQQSYKSLVQIHEKNGWYTPPKEDG
Disclosure; SEQ ID NO 5340; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 1020.5; DB 49.0%; Pred. No. 4.1e-78; tive 72; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLPOHPDVEMLDQPLPAEQCTQEDVSSEDE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                (ABB57737-ABB72072).
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Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       397 AA
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 PVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANKS---Q 392
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVS
Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 27855; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 808; DB 22; Length 272.4%; Pred. No. 2e-60;
Live 31; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB60719 standard; Protein; 306 AA.
                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                             2000US-191637P.
2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 152; Conservative
                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                               /enter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
N-PSDB; ABL11124.
                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 AA;
                                                                                                      WO200171042-A2
                                                                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nteractions
                                                                                                                                              7-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corresponding nucleic acid. The invention also relates to methods for treating, diagnosing, preventing and screening for disorders related to the expression of RATLide. UBC is useful for screening for candidate compounds capable of binding to and/or modulating its activity. UBC is useful for treating an immune or neuronal disorder in a mammal. The method is useful for treating a cancer or tumour. It is useful for screening for neuronal disorder in a suppression. It is also useful for treating lymphoproliferative disorder. Cancer e.g. adenocarcinoma, leukaemia, myeloma, sarcoma, etc, neurodegenerative disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma, multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's disease, dementia, depression, etc, immune disorder or immune related disorders such as acquired immuno deficiency syndrome (AIDS), allergy, anaemia, atopic dermatitis, diabetes mellitus, myccardial infarction, etc, developmental disorders e.g. Cushing's syndrome, renal the present sequence is human RATLid6 UBC domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ubiquitin conjugating enzyme polypeptide isolated from activated human T cell, for screening modulators useful for treating cancer, immune disorder, lymphoproliferative disorder, neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 GSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 834; DB 23;
100.0%; Pred. No. 8.4e-63;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                              Finger JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 167; 169pp; English.
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                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                29-OCT-2001; 2001WO-US46559.
                                                                                                                                                        30-OCT-2000; 2000US-244688P.
30-JUL-2001; 2001US-308706P.
                                                                                                                                                                                                                                                        Bowen MA, Wu Y, Yang W,
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                                   WO200236741-A2.
Homo sapiens.
                                                                           10-MAY-2002
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Drosophila melanogaster,
                             WO200171042-A2
                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                      interactions
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                                                27-SEP-2001
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                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent explains 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                       228 AILEKIKKNQRQDY-----LNGAVSGSVQATDRIMKELRDIYRSQSFKGGNYAVEL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANK----SQYS 394
                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                  Length 306;
                                                                                                                                                                                                                              Disclosure; SEQ ID NO 8949; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 440.5; DB 22; 45.2%; Pred. No. 6e-29; iive 41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
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                                                                                                                                             PWD,
                                                                                             2000US-191637P.
2000US-0614150.
                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                         New isolated nucleic acid
genes from Drosophila and
interactions
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity 45.2 94; Conservative
                  Drosophila melanogaster.
                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL04822.
                                                                                                                                                                                                                                                                                                               (ABB57737-ABB72072)
                                                                                                                          NY
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pharmaceutical
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11-JUL-2000;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 IEKGYVMEGGAICMELLTPRGWASAYTVEAVIMQFAASVVKGQGRI---ARKPKSTKEFT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANK----SQYS 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: | :|||: | |||||
107 AVWDSPGKRRRQDHKVAPTTERQLVAAPDHTIR-TRRIMKEYREMERLQAKNDAVFTVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AILEKIKKNQRQDY-----LNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 8958; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discloses genomic DNA sequences (ABL16176-ABL30511), exsequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 RRQAEESFRSLVKTHEKYGWVTPALSDG 306
                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 LTRAQQSYKSLVQIHEKNGWYTPPKEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic protein #11960.
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                                                                                                                                                                                                         Li PWD,
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                                                         2000US-191637P.
2000US-0614150.
23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 94; Conserva
                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL04825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                             (PEKE ) PE CORP NY
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Matches
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CR diagnostic amino acid sequences of the Invention of well sequences of the Invention.

CR diagnostic amino acid sequences of the Invention of appear in the printed activity and the specification, but was obtained in electronic format directly from Wipo at the Invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 LYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VQATDRLMKELRDI-----YRSQSFKGGNYAVELVNDSLYDWNVK-----L 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 GDPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 WM-----FEMLDQPLPMGQNGKIEVTSEEEEEEWAGDIKYLNHCKWKKEELISGKKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 DEGIEKENLATLEKIRKTQSQCHLNVMWCLGSGETTKPRNSGSTGRRKESKQLKAGSQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   mutations
                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.7%; Pred. No. 8.8e-17;
Matches 89; Conservative 30; Mismatches 62; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 DDGIGKENLAILEKIKKNQRQDYLN:----GAV----SGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 42328; 103pp; English.
                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                            30-MAR-2001; 2001WO-US08631
                                                                                                                                                                     2000US-0540217
2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 LNREOEERL 441
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N-PSDB; AAS76156.
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                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                      WO200175067-A2
Homo sapiens.
                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                 11-0CT-2001
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polymetrase chain reaction (FKS) primare (1) and probes, polymetrase chain reaction (FKS) primare, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The control of (II) and in recombinant production of (II). The control activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and canding actic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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63.5%; Pred. No. 2e-13;
... Wismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 58592; 103pp; English.
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                                                                                                                                                                                                              Novel human diagnostic protein #28224.
ABG28233 standard; Protein; 400 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
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                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                        18-FEB-2002
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                                                                      ABG28233;
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170 MLDQPLPAEQ 179. 183 MPDQPLPMGQ 192

us-10-005-549-2.rag

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Claim 20; SEQ ID No 45893; 103pp; English.
333 MLDQPLPTGQNGTTEEVTSEEEEE 357
                                                        Novel human diagnostic protein #15525
                         ABG15534 standard; Protein; 1909 AA
                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                          31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                              (first entry)
                                                                                                                                                              WPI; 2001-639362/73.
N-PSDB; AAS79721.
                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                            WO200175067-A2.
                                                                                  Homo sapiens.
                                                                                                                                                                                              biodiversity
                                              18-FEB-2002
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                                   ABG15534;
               RESULT 15
                    ABG1553
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappositios, for genefic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human confidence of the print of any properties of the print of manners in the printed
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110 ESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVE 169 

8.4%; Score 187.5; DB 22; Length 1909; 58.6%; Pred. No. 2.7e-06; Live 7; Mismatches 21; Indels 1;

Query Match Best Local Similarity 58.69 Matches 41; Conservative

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1; Gaps

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Search completed: July 29, 2003, 13:44:52
Job time: 85 secs
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OM protein - protein search, using sw model

July 29, 2003, 13:42:28 ; Search time 42 Seconds (without alignments) 966.266 Million cell updates/sec Run on:

US-10-005-549-2
2229
1 MQDPQPQGQQDGGQDGG......KSLVQIHERNGWYIPPKEDG 422 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	ubjaultin-conjugat	probable immediate	HBRM protein - him	ubjauitin-protein	SNF2alpha protein		potassium channel					ubiquitin conjugat	O		protein BRG1 - hum	hypothetical prote	m cha	antigen, p83/100 h		glutamic acid-rich	collagen alpha 1(X	ryanodine receptor	hypothetical prote	RESA-H3 antiqen PF	hypothetical prote	initiation factor	SNF2beta protein -	ryanodine receptor
SUMMARTES	ID	T21349	A41241	T03166	839580	T08465	S45251	B70694	S12746	F90082	F90118	F90137	D90102	<b>Н90116</b>	T20410	C86725	839059	T00367	B41359	G70192	A59437	A40437	S23810	B35041	T33074	B71603	D96541	F87103	S45252	146646
	DB	7				C4		7	7	7	7	7	7		7	a	~	7	7	7	7					7		7	~	-
	Query Match Length DB	471	295	1300	1586	199	1572	900	924	147	147	147	147	147	382	924	1613	756	924	700	1445	290	1603	5037	1262	1558	195	924	1647	5035
dР	Ouery Match	37.7	6.1	-	٠.	5.9	5.8	5.5		5.5	ທຸ	5.5	5.5	5.5	5.4	5.4	5.4	5.4	5,3	5	ω 	5.3	5.3	5.2	5.5	5.2	5.2	5.2	5.5	5.2
	Score	841	135.5	133	132.5	131	129.5	123.5	122	121.5	121.5	121.5	121.5	121.5	120.5	120.5	120.5	120	119	118.5	.118.5	117.5	117.5	1117	116.5	116.5	116	116	116	115.5
	Result No.	1	7	ო	4	ς.	9	7	ω.	σ ;	10	11	12	13	14	15	16	17	18	19	20	77	22	23	24	25	56	27	28	53

97K alpha trans-in ryanodine receptor	hypothetical prote G-protein signalin	myosin neavy chain hypothetical prote transforming prote	transforming proce	bHLH transcription endopeptidase La h	hypothetical prote ubiquitin-conjugat	ubiquitin conjugat hypothetical prote	bifocal protein -
TNBEA1 A35041	S67248 S78089	T27167 S20099	TVHUME	G84545 S57342	T23820 A48145	I39202 T48719	T03743
ਜਂਜ	000	900	0	7	77	77	7
871 5032	156	152	364	467	147	147 751	. 1063
5.2			0.0	50.0	5.0	5.0	5.0
115	114	113.5	112.5	112	111.5	111.5	111.5
30 31	332	323	37	39	41 42	4 4 4 4	45

# ALIGNMENTS:

sgans 99 #text_change 04-Mar-2	96	DBJ. ; GSPDB:GN00019; CESP		al protein F25H2.8
RESULT 1 T21349 hypothetical protein F25H2.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C;Accession: T21349	R;Wilkinson, J. submitted to the EMBL Data Library, September 1996 A;Reference number: 219411 A;Accession: T21349	A:Status: preliminary; translated from GB/EMBL/DDBJ. A:Nolecule type: DNA A:Residues: 1-471 < WIL> A:Cross-references: EMBL:Z79754; PIDN:CAB02096.1; GSPDB:GN00019; CESP:F25H2.8	A; Experimental source: clone F25H2 C; Genetics: A; Gene: CSES: F25H2.8	A; Introns: 26/3; 138/3; 302/3; 353/3; 379/2 C; Superfamily: Caenorhabditis elegans hypothetical protein F25H2.8

Gaps 52; Ouery Match 37.7%; Score 841; DB 2; Length 471; Best Local Similarity 44.9%; Pred. No. 6.9e-46; Matches 180; Conservative 69; Mismatches 100; Indels

10;

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C;Accession: S39580
B;Muchardt, C.; Yaniv, M.
EMBO J. 12, 4279-4290, 1993
A;Title: A human homologue of Saccharomyces cerevisiae SNF2/SW12 and Drosophila brm g A;Reference number: S39580; MUID:940389j0; PMID:8223438
A;Accession: S39580
                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Moleddes: 1-1300 < CENS
A;Residues: 1-1300 < CENS
A;Cross-references: EMBL:AF005370; NID:92337967; PIDN:AAC58118.1; PID:92338034
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl:terminal homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PQGQQQPGP----GQQL-----GGQGAAPGAGGGPGGGP-GPGPCLRRELKLLESIFHRG 55
                                                                                                                                                           probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan:1995 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1586 <->AUC>
A; Residues: 1-1586 <->AUC>
A; Cross-references: EMBL: X72889; NID: 9414116; PIDN: CAA51407.1; PID: 9414117
C; Superfamily: human SNF2alpha protein; bromodomain homology
E; 216-249/Region: glutamine-rich
F; 1423-1478/Domain: bromodomain homology <->BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QPQPQGQQQP-----GPGQQLGGQGA----APGAGGGPGGPGPGPCLRRELKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 QOVPKGAEGSEGEGPCR----PGGPDEDGDPEGPDGTEGEGPCGPGGPDEDGDPEGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQE--DVSSEDEDEEMPEDTEDLDHY
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                                                                                                                                                                                                                                                                     R; Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Tille: Primary structure of the alcelaphine herpesvirus .1 genome.
A;Reference number: Z14840; WUID:97404659; PMID:9261371
A;Accession: T03166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 OPQTQQQQPALVNYNRPSGPGPELSGPSTPQKLPVP----APGGRPSPAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 133; DB 2; Length 1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 PEGECQSGPSSCEGQQVPKGPDGPEEGSSGPGSSEGEGPSGPGS----
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22.0%; Pred. No. 2.8;
ive 39; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMKEEEPAEGKKSEDDGIGKENLAIL 230
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| || :| NKDMADNFWYDSDLDD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.48;
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Matches 65; Conservative
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Matches 68; Conserv
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A;Molecule type: mRNA
A;Residues: 1-1586 <M
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                             196
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A, Residues: 1-295 <-BRA.

A, Cross-references: EMBL: X84162; NID: 9706817; PID: 9706820

R, Brandt, P.; Ramlow, S.; Otto, B.; Bloecker, H.

Yeast 12, 85-90, 1996

A, Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacchard

A, Reference number: S61741; MUID: 96381250; PMID: 8789263
                                                                                                ubjuitin-conjugating enzyme CDC34 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D4211; protein YBRD295; protein XD9609.08c; protein YDR054c;
Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 22-3nn-1993 #sequence_revisiae
C;Accession: A41241; S54038; S58834; S61743; S67870
C;Accession: A41241; S54038; S58834; S61743; S67870
A;Title: The yeast cell cycle gene CDC34 encodes a ubjquitin-conjugating enzyme.
A;Reference number: A41241; MUD:88321694; PMID:2842867
A;Residues: 1-295 GGE>
A;Residues: 1-295 GGE>
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A; Residues: 1-295 <BLO-
A; Cross-treferences: EMBL:274350; NID:g1431496; PID:e253311; PID:g1431497; MIPS:YDR054c
A; Experimental source: strain S288C
C; Genetics:
A; Gene: SGD:CDG34; UBG3
A; Cross-references: SGD:S0002461; MIPS:YDR054c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-295 < BRW>
A; Residues: 1-295 < BRW>
A; Cross-references: EMBL: X84162; NID:g706817; PIDN:CAA58970.1; PID:g706820
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
B; Bloccker, H.; Brandt, P.
B; Bloccker, H.; Brandt, P.
A; Reference number: S67587
A; Reference number: S67870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 STHIELEDDSNIFTWNIGYMVLNEDSIXH------GGFFKAQMRFPEDFPFSPPQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 NYAVELVNDS-LYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Cross-references: GB:M21877; NID:g173123; PIDN:AAA35188.1; PID:g173124 A)Note: the authors translated the codon ATA for residue 50 as Ala R; Hunt, S.; Bowman, S.; Harris, D. Submitted to the EMBL Data Library, May 1995
A; Reference number: S54031
A; Reference number: S54031
A; Residues: 1-295 <HUN>
A; Residues: 1-295 <HUND:g798897; PID:g798905
A; Reference number: S58832
A; Reference number: S58832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VKGKARVQFGANKSQYS----
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S61743
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C; Keywords: nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S58834
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49 ESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAAPGPHLPPRGSVPGDPVRIHCNI 288	A; Residues: 1-1572 <chi> A; Residues: 1-1572 <chi> C; Superifamily: Numan SYF2alpha protein: bromodomain homology F; 1409-1464/Domain: bromodomain homology <sro></sro></chi></chi>
DD 318 QQKQSRISPIQKPQGLDPVEILQEREYRLQ-ARIAHRIQELENLPGKPPP 366	h 15
OY 167 DVEMLDOPLPAEQCTQEDVSSEDEEMPEDTEDLDHYEMKEEEPAEGKKSE 218	lsmatch .GGQGA-
219	Db 245 QPQTQQQQQPALVNYNRPSGPGPELSGPSTPQXLPVPAFGGRPSPAP 291
427 KLEKQOKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVAGKIQK	49 ESIFHRGHERFRIASACLDELSCEFL
Qy 279 VNDSLYDWN 287	292
Db 472 LSKAVATWH 480	QY 109 TESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHP 166  121
RESULT 5	167 DVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSE
ubiquitin-protein ligase (EC 6.3.2.19) - fruit fly (Drosophila melanogaster) N;Alternate names: ubiquitin conjugating enzyme	DD 371 DERTKATVELKALRILINFORQLREEVVACMRRDTILETALNSKAYKRSKRQTLREARWTE 430
C;Species: Drosophila melanogaster C;Date: 11-Jun-1999# sequence_revision 11-Jun-1999 #text_change 03-Jun-2002 C;Accession: T08465	GNYAVEL
R;Kirby, R.J. submitted to the EMBL Data Library. June 1996	1 0
A; Reference number: 216421	:  :: ::
A; Status: 100%; translated from GB/EMBL/DDBJ A; Oblecule type: mRNA	Db 476 LSKAVATWH 484
A; Residues: 1-199 KIRS A: Cross-references: RMR: V92838: NID: 412566513: DID: 41054703	RESULT 7
A:Experimental source: strain Canton-S C;Genetics:	B70694 probable infB - Mycobacterium tuberculosis (strain H37RV)
A; Gene: Ubcot A; Cross-references: FlyBase:FBgn0015321	<pre>C:Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Feb-2001 C;Accession: B70694</pre>
C;Superiamity: Yeast wightith Procein ligase UBC! C;Keywords: cell cycle control; DNA repair; ligase; protein degradation	
Query Match 5.9%; Score 131; DB 2; Length 199; Best Local Similarity 24.7%; Pred. No. 0.21; Matches 38; Conservative 32; Mismatches 56; Indels 28; Gaps 7;	<pre>kajandream, M.A.; Kogers, J.; Kutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Ittle: Deciphering the biology of Mycobacterium tuberculosis from the complete genc</pre>
252	0500; MUID:98295987; PMID:9634230
Db 5 AVSRIKREFKEVARSEEIVQCSIKIELVNDSWTELRGEIAGPPDTPY 51	ומכופדר מכום מכלתפוורם ווסר מווסאווי
OY 310 EGADFILLNFSFKDNFPFDPPFVRVVSPYLSGGYVLGGGAICMELLTRQGWSSAXSIESV 369	A; Mesidues: 1-900 CCOL> A; Mesidues: 1-900 CCOL> A; Cross-references: GB:281331; GB:AL123456; NID:g3261650; PIDN:CAB03670.1; PID:g16486 A; Experimental source: strain H37Rv C; Genetics:
370	A.Gene: infB C.Superfamily: translation initiation factor IF-2; translation elongation factor Tu P. C.Kevwords: GTP binding: nucleotide binding: P-loon
DD 110 LESLQALLAAAEPDDPQDAVVAYOFKDKYDL 140	F;399-512/Domain: translation elongation factor Tu homology <etu> F:405-412/Region: nucleotide-binding motif A (P-loop)</etu>
RESULT 6 S45251 SNF2alpha protein - human	F;5U9-51Z/Region: GTP-binding NKXD motif F;545-547/Region: GTP-binding SAK/L motif F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser
C; Species: Homo sapiens (man) C; Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002 C; Accession: \$4521.	Query Match 5.5%; Score 123.5; DB 2; Length 900; Best Local Similarity 20.5%; Pred. No. 4.9; Matches 92; Conservative 63; Mismatches 128; Indels 165; Gaps 21;
Nucleic Acids Res. 22, 1815-1820, 1944 A; Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila brahm A; Reference number: S45251; MUID:94268902; PMID:8208605	QY 4 PQPQGQQ-QPGPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLESIF 52
A; Status: preliminary A; Molecule type: mRNA	QY 53 HRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRG 95

Db 261	Db 331 FDRHPKSFSSILNFYRTGKLHIVDEMCVLAFGDDLEYWGVDELYLESCCQHKYHQRKENV 390
QY 96SVPGDPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQ 147 :  1:	OY 192 -EEMPEDIEDLDHYEMKEEEPAEGKKSE 218 
QY         148 HLKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMK 207           : : : : : : : : : : : : : : : : : : :	RESULT 9 F90082 ubiquitin conjugating enzyme [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
QY 245AVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKV 293	C.Accession: F90082 R.Bouglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Nature 410, 1091-1096, 2001 A.Title: The highly reduced genome of an enslaved algal nucleus.
QY: 294 DQDSALHNDLQILKEKEGADF-ILLNFSFKDNFPEDPPFVRVVSFVLSGGYVLGGGA 349    1	A; Reference number: A9908; MUID:113230/1; PMID:113230/1 A; Status: preliminary A; Molecule type: DNA
QY 350 ICMELLTRQGWSSAYSIBSVIMQISATL 377  1 :::	A; Kestoucus: 1.147 CDOUZA A:Cross references: GB:AF165818; NID:g6690600; PIDN:AAF24208.1; GSPDB:GN00150 C; Genetics: A; Gene: ubc4
RESULT 8	A;Genome: nucleomorph C;Superfamily: human ubiquitin-protein ligase E2 C;Keywords: nucleomorph
potassium channel protein shabil - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999 C;Accession: S12746; S15058	Query Match 5.5%; Score 121.5; DB 2; Length 147; Best Local Similarity 25.3%; Pred. No. 0.56; Matches 39; Conservative 29; Mismatches 59; Indels 27; Gaps 7;
R;Butler. A.; Wel, A.; Salkoff, L. Nucleic Acids Res. 18, 2173-2174, 1990 A;Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila. A;Reference number: S12746; MUID:90245668; PMID:2336395	QY 252 ATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEG 311
A, Molecule type: mRNA A; Mesidues: 1-924 <but> A; Cross-references: EMBL:M32659</but>	QY 312 ADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGNSSAYSIESVIM 371
R;Butler, A.; Wei, A.; Salkoff, L. submitted to the EMBL Data Library, March 1990 A;Description: Shal, Shab, and Shaw: Three genes encoding potassium channels in Drosophi A;Reference number: S15058 A;Accession: S15058	Qy 372 QISATLVKGKARVQFGANKSQYSLT 396 
A; Molecule type: mRNA A; Residues: 1-625, YG', 628-924 <bu2> A; Cross-references: EMBL:M32659; NID:g158458; PIDN:AAA28896.1; PID:g158459 C; Genetics: A; Gene: Shabil A; Cross-references: FlyBase: FBgn0003383 C; Superfamily: potassium channel protein drkl C; Keywords: ion channel, potassium channel; transmembrane protein</bu2>	.ph ymbiont Tun-2001
Query Match 5.5%; Score 122; DB 2; Length 924; Best Local Similarity 23.9%; Pred. No. 6.3; Matches 64; Conservative 27; Mismatches 101; Indels 76; Gaps 12;	R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Nature 410, 1091-1096, 2001 A;Title: The highly reduced genome of an enslaved algal nucleus. A;Reference number: A99082; MUID:11323671; PMID:11323671
OY 13 GPGOOLGGGGAAPGAGGGPGGGPGCP-CLRRELKLLESIFHRGHERFRIASACLD-ELS 70	A; Accession: Politio A; Status: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-147 < DOU> A; Cross references: GB: AF083031; NID: 96690139; PIDN: AAF24004.1; GSPDB: GN00152
214 SQQIVGGVGGVGGASSQSISGGVPTHSQSNTTGALQRTHSRSMSSIPPPEPFMIAQ 123 SDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNL	A;Gene: ubc4 A;Map position: 3 A;Geneme: nucleomorph C;Superfamily: human ubiquitin-protein ligase E2 C;Keywords: nucleomorph
Db 272 SKAVNSRVSINVGGVRHEVLWRTLERLPHTRLGRLGECTTHEAIV-ELCDDYSLADNEYF 330 Qy 163 -PQHPDVEMLDQPLPAEQCTQEDVSSEDED- 191 :: :	Query Match 5.5%; Score 121.5; DB 2; Length 147; Best Local Similarity 25.3%; Pred. No. 0.56; Matches 39; Conservative 29; Mismatches 59; Indels 27; Gaps 7;

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C; Accession: H90116
R; Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Nature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                              252 ATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEG 311
                                                                                                                                                                                                                                                                              312 ADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIM 371
                                                                                                                                                                                                                                                                                                             GGVFFLSILFPPDYPFRPPKYQFTTKIYHPN-INSNGSICLDILRDQ-WSPALTVSKVLL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AJ010592; NID: g12580795; PIDN: CAC27113.1; GSPDB: GN00151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 ADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIM 371
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ubiquitin conjugating enzyme [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Gillardia theta A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                             Gaps
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                                                                             Length 147;
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                                                                        5.5%; Score 121.5; DB 2;
25.3%; Pred. No. 0.56;
Live 29; Mismatches 59;
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dlarity 25.3%; Pred. No. 0.56;
Conservative 29; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                 372 QISA-----TLVKGKARVQFGANKSQYSLT 396
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A; Reference number: 219271
A; Accession: 720410
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1385 <#IL>
A; Cross-reference
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C;Keywords: nucleomorph
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Matches 39; Conserv
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A; Molecule type: DNA
A: Residues: 1-147 < DOU>
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Best Local Similarity
Matches 39; Conserv
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A; Note: a nucleomorph Guillardia theta
A; Note: a nucleomorph Guillardia theta
A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C; Accession: F90137
R; Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671; PMID:11323671
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A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C;Accession: D90102
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Fylature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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C;Genetics:
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| Cross-references: GB:AJ010592; NID:912580660; PIDN:CAC26977.1; GSPDB:GN00151
                                                                                                                                                    252 ATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 ADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLIKQGWSSAYSIESVIM
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                                                                                                                                                                                                                                                                                                                                                                                                ubiquitin conjugating enzyme [imported] - Guillardia theta nucleomorph
                                                                   2 ATKRICKEHKDLLKDPP---SNCSAGPSDENLFRWTASIIG-PSDSPY----
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25.3%; Pred. No. 0.56;
ive 29; Mismatches
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C;Superfamily: human ubiquitin-protein ligase E2
C;Keywords: nucleomorph
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A;Molecule type: DNA
A;Residues: 1-147 <DOU>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-147 <D01
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Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss Reference number: A86625; MUID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <STO>
A;Cross:references: GB:AE005176; PID:g12723724; PIDN:AAK04901.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 NLAAVLE----RLVDIKKGNTLLL---QHLKRIISDL-CKLYNLPQHPDVEMLDQPLPAE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 FLLAGAGGAGAAPGPHLPPRGSVPGDPVRIHCNITESYPAVPPIWSVESDDPNLAAVL 132
                                                                                                                                                                                                                                                                                                                               ---GGGGGGGGGGGGGRKKREAINVYGHDDLNKCNNEEL----RIILNENTKETVAESI 230
                                                                                                                                                                                                                                                                                                                                                                        133 ERLVDIKKGNTLLL-----QHLKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQEDVS 186
                                                                                                                                                                                                                                                                                                                                                                                                                231 KTLKEKVAGODYIVVCNEKPAPFTAETDDFCSLOKENVHCTILRINHKEVAEK-NEEDKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --QCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKK- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NORODYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVE----LVNDSLYDWN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKLLKVDQDSALHNDLQILKEKE-----GADFILLNFS-----FKDNFPFDPPFVRV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLESIFHRGHERFRIASACLDELSCE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss: Lactococcus lactis subsp. lactis
23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 SED--EDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Gaps
                                                                                                                                                                         Gaps
                                                                                                                                                                       53;
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                                                                                                                              Length 385;
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                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                          Query Match 5.4%; Score 120.5; DB 2; Best Local Similarity 22.9%; Pred. No. 2.4; Matches 54; Conservative 28; Mismatches 101;
                                                                                                                                                                                                                                                151 GGGGCGGGGGGGGGGGGGGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 120.5; E; Pred. No. 7.8; 41; Mismatches
                                      A; Gene: CESP:E02A10.2
A; Map position: 5
A; Introns: 32/1; 72/1; 85/1; 122/1; 133/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: July 29, 2003, 13:47:59 Job time: 44 secs
A, Experimental source: clone E02Al0 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%
Best Local Similarity 24.2%
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 VSPVLSGG 342
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OM protein .- protein search, using sw model

July 29, 2003, 13:35:48 ; Search time 23 Seconds (without alignments) 862.838 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-005-549-2
2229
1 MQPQPQGQQPGPGQQLGG......KSLVQIHERNGWYIPPKEDG 422

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		:	omyc	sapien	culu	norv	teri	ila	sol	psis	musculu	sapien	sapien	sapien	sapien	ila	lae	ırus	sapien	agus	culu	teri	pien	sapten	ofa	herp	pien	·omyc	pien	omyc	alb	io sa	gall	sapien	culu
	tion		saccharomyc	homo sa	mus musculu	rattus norv	mycobacteri	drosophila	spisula sol	arabidopsis	snw snw	homo	homod	рошо	homo	drosophila	xenopus lae	bos taurus	homo sa	oryctolagus	mus musculu	mycobacteri	homo sapien	homo sa	sus scrofa	equine herp	homo sapien	saccharomyc	homo sapien	saccharomyc	candida	medicago sa	gallus gall	homo sa	mus musculu
	Description		P14682	P51531	P52483	099m76	P71613	P52486	095044	004379	P52482	075154	09y5b6	P51965	096kg7	P17970	P56616	028181	201092	P11716	09z148	09z519	P51532	P54257	P16960	P28929	P21817	P52492	P49796	P08964	074201	P35130	P27921	P12524	035613
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T T T T T T T T T T T T T T T T T T T	8		UBC3_YEAST	SN22_HUMAN	TB6B_MOUSE	SA3_RAT	IF2_MYCTU	UBC4_DROME	UBCB_SPISO	AGO1_ARATH	UBC6_MOUSE	EFER_HUMAN	GCFC_HUMAN	UBC6_HUMAN	BAT8_HUMAN	CIKB_DROME	UBCB_XENLA	CNG4_BOVIN	CA1F_HUMAN	RYR1_RABIT	BAT8_MOUSE	IF2_MYCLE	SN24_HUMAN	HAP1_HUMAN	RYR1_PIG	UL47_HSVEB	RYR1_HUMAN	UBCA_YEAST	RGS3_HUMAN	MYS1_YEAST	UBC2_CANAL	UBC2_MEDSA	JUND_CHICK	MYCL_HUMAN	DĄXX_MOUSE
	DB	1 1 1		-	Н	-					-	-	_		7	-	-	-	7	7	Н	-	٦	-		-	-	Н	H		-	-		7	-
	Query Match Length		295	1586	207	1256	006	199	177	1048	193	756	917	193	1210	985	179	1394	1603	5037	1263	924	1647	671	5035	871	5038	156	519	1928	179	152	323	364	739
æ	Query Match	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	6.1	٠	٠	•	٠	5.5	٠	5.5	5.5	5.4	5.4	5.4	5.3	5.3	ы Э.	5.3	5.3	5.2	•	2.5	•	5.2	5.2	2.5	5	5.1	5.1	5.1	5.1	5.0	5.0	5.0	5.0
	Score	1	135.5	132.5	129.5	125.5	123.5	123	122.5	122.5	121.5	120	$\sim$	119.5	118.5	118	117.5	117.5	117.5	117	116.5	116	116	115.5	115.5	115	114.5	114	114	114	113	112.5	112.5	112.5	112.5
	Result No.		-	7	m)	4	'n	9	7	ω.	o j	10	11	12	13	14	15	16	17	18	19	20	21	22	53	24	25	26	27	. 28	53	30	31	32	33

P51668 homo sapien P5129 caenorhabdi Q91al2 gallus gall Q9q02 rattus norv Q9uer7 homo sapien P42746 arabidopsis P15732 saccharomyc P35134 arabidopsis P46936 gallus gall Q06846 bos taurus Q35668 mus musculu P25867 drosophila
UB5A_HUMAN UBC2_CAEEL VSX1_CHICK S511_RAT DAXX_HUMAN UBC3_ARATH UBC5_YEAST UBCB_ARATH YAP1_CHICK RP3A_BOVIN HAP1_WOUSE UBC1_DROME
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## ALIGNMENTS

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| :| : | :| :| :| 37 FR-FTPAIXHPNVYRDGRLCISILHQSGDPMTDEPDAETWSPVQTVESVLISIVSLLEDP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VKGKARVQFGANKSQYS------410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NINSPANYDAAVDYRKNPEQYKQRVKMEVERSKQDIPKGFIMPTSESAYISQSKLDEPES 195
                                                                                                                                                                                                                                                                                                                                                                                                                                  273 NYAVELVNDS-LYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 VRVVSPVLSGGYVLGGGAICMELLTKQG------WSSAYSIESVIMQISATL--- 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 SFHIELEDDSNIFTWNIGVWVLNEDSIYH------GGFFKAQMRFPEDFPFSPPQ 76
                                                                                                                                                                                                                                                                                                                                                                                                    59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chiba H., Muramatsu M., Nomoto A., Kato H.;
Chiba H., Muramatsu M., Nomoto A., Kato H.;
"Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and
Drosophila brahma are transcriptional coactivators cooperating with
the estrogen receptor and the retinoic acid receptor.";
Nucleic Acids Res. 22:1815-1820(1994).
                                                                                                                                                                                                               PROSITE: PS00183: UBIQUITIN_CONJUGAT_1; 1.
PROSITE: PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ubl conjugation pathway; Ligase; DNA replication; Nuclear protein; Cell cycle; Cell division; Multigene family.
BINDING 95 95 95 95 95 95 AS/GLU-RICH (ACIDIC).
SEQUENCE 295 AA; 34064 MW; ICE3E0C3AB1436DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muchardt C., Yaniv M.;
"A human homologue of Saccharomyces cerevisiae SNF2/SWI2 and
Drosophila brm genes potentiates transcriptional activation by the
glucocorticoid receptor.";
EMBO J. 12:4279-4290(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                             PIR; A41241; A41241.
HSSP; Q02159; 2UCZ.
SGD; S0002461; CDC34.
GO; GO: Q0000066; PGZ/M transition of mitotic cell cycle; IPI.
InterPro; IPR000668; UBQ_conjugat.
PF00179; UQ_con; 1.
Probom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
8-FERB-2003 (Rel. 41, Last annotation update)
POSSIBLE global transcription activator SNF2L2 (SNF2-alpha).
SWARCA2 OR SNF2L2 OR BRW OR SNF2A.
                                                                                                                                                                                                                                                                                                                                                                Query Match 6.1%; Score 135.5; DB 1; Length Best Local Similarity 21.4%; Pred. No. 0.11; Matches 42; Conservative 33; Mismatches 62; Indèls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1586 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKDMADNFWYDSDLDD 211
                                              CAA98872.1; -. CAA89083.1; -.
              EMBL; M21877; AAA35188.1;
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                                                                                                                                                                                                        SM00212; UBCc; 1
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                                                274350;
                                  X84162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
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P51531;
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                                                EMBL;
EMBL;
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entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@lsb-slb.ch).
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QPQPQGQQQP-----GPGQQLGGQGA----APGAGGGPGGGPGPCLRRELKLL
-1- FUNCTION: TRANSCRIPTIONAL COACTIVATOR COOPERATING WITH NUCLEAR HORMONE RECEPTORS TO POTENTIATE TRANSCRIPTIONAL ACTIVATION.
-1- SUBCELLUIAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iranscription regulation; Nuclear protein; Activator; Bromodomain;
ATP-binding; Helicase; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 600014; -. GO CONTROL CON
                                                                                                                                                                                                               -1- SIMILARITY: Contains 1 bromodomain.
-1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135 1135 D -> H (IN REF. 2).
1390 1390 C -> V (IN REF. 2).
1586 AA; 180762 MW; FA537F2A2392807A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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-> PQQQP (IN REF. -> S (IN REF. -> S (IN REF. -> S (IN REF. -> S).
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DEGH BOX.
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22.0%; Pred. No. 1.6;
ive 39; Mismatches
                                                                                                                                                                                       IsoId=P51531-2; Sequence=VSP_000577;
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BROMODOMAIN.
                                                                                                                                            IsoId-P51531-1; Sequence-Displayed;
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POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001410; DEAD.
InterPro; IPR001650; Hellcase_C.
InterPro; IPR000565, HSA.
InterPro; IPR000330; SNF2_N.
Pfam; PP00439; bromodomain; 1.
Pfam; PP00439; bromodomain; 1.
Pfam; PP00176; SNF2_N; 1.
PRINTS; PR05051; HRDMODOMAIN.
SWART; SM00597; BRRMODOMAIN.
SWART; SM00497; BRDMO; 1.
SWART; SM00497; BRDMO; 1.
SWART; SM00497; HSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X72889; CAA51407.1; -. EMBL; D26155; BAA05142.1; -. PIR; S39580; S39580. Genew; HGNC:11098; SMARCA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Conservative
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                                                                                                                    Name-Long;
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                                                                                                                                   426
ESIFHRGHERFRIASACLDELSCEFLLAGAGGAGAAAPGPHLPPRGSVPGDPVRIHCNI 108
                                                                                                                                                                                     471
                 109 TESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQH--P
                                                                       QXQSRISPIQKPQGLDP-----VEILQEREYRLQ--ARIAHRIQELENLPGSLPP
                                                                                                       D----VEMLDQPLP--AEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSE
                                                                                                                              DIRTKATVELKALRLINFOROLROEVVACMRRDTTLETALNSKAYKRSKROTLREARMTE
                                                                                                                                                        DDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRIMKELRDIYRSQSFKGGNYAVEL
                                                                                                                                                                           427 K--LEKOQKIEQERKRRQKHQEYLNSILQHA------KDFKEYHRSVAGK-----IQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphosphate + protein N-ubiquityllysine.
PATHWAY: Ubiquitin conjugation; second step.
MISCELLANEOUS: A cysteine residue is required for ubiquitin-thiolester formation (By similarity).
SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matuschewski K., Hauser H.P., Treier M., Jentsch S.;
Tdentification of a novel family of ubiquitin-conjugating enzymes
with distinct amino-terminal extensions.",
J. Biol. Chem. 271:2789-2794(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pestov D.G., Grzeszkiewicz T.M., Lau L.F.;
"Isolation of growth suppressors from a cDNA expression library.";
Oncogene 17:3187-3197(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine - AMP
                                                                                                                                                                                                                                                                                                                                   vi-ucr-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubquitin-conjugating enzyme E2-23 kDa (EC 6.3.2.19)
(Ubquitin-protein ligase) (Ubiquitin carrier protein).
UBCE4 OR UBCM2.
                                                                                                                                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:107412; Ubce4.
InterPro; IPR000608; UBQ_conjugat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99087339; PubMed-9872334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96162026; PubMed-8576256;
                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF003346; AAB60948.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X92664; CAA63352.1;
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                  472 LSKAVATWH 480
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                        279 VNDSLYDWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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STATANAWAREAUS.

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SA BAYES W. Prieto I., Noguchl J., Barbero J.L., Perez Jurado L.A.;

Bayes M., Prieto I., Noguchl J., Barbero J.L., Perez Jurado L.A.;

Bayes M., Prieto I., Noguchl J., Barbero J.L., Perez Jurado L.A.;

R. "Evaluation of the Stag3 gene and the synaptonemal complex in a rat

model. (as/as) for male infertility.";

Mol. Reprod. Dev. 60:414-417(2001).

-!-PUNCTION Molosis specific component of cohesin complex. The cohesin complex is required for the cohesin complex represented can be a large proteinaceous ring within which sister chromatids can be trapped. At anaphase, the complex is cleaved and dissociates from chromatin, allowing sister chromatids to segregate. The meiosis-

C Specific cohesin complex probably replaces mitosis specific cohesin complex when it dissociates from chromatin during prophase cohesin complex likely contains RAD21, or the meiosis-specific cohesin complex likely contains RAD21, or the meiosis-specific complex likely contains RAD21, or the meiosis-specific corpus and protein REC8 (By similarity).

C Such complex likely contains RAD21, or the meiosis-specific corpus and protein REC8 (By similarity).

C I SUBCELLUIAR LOCATION: Nuclear protein. Associates with chromatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 SGSVQA-----TDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 SEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNORODYLNGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDDESPSTSSGSSDAD----QRDPAAPKPEEQ------EERKPSATQQKKNTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 SSKTTAKLSTSAKRIQKELAEITLDPP---PNCSAGPKGDNIYEWRSTIL--GPPGSVY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cohesin subunit SA-3 (Stromal antigen 3) (SCC3 homolog 3).
                       Fromom; PD000461; obc._.
SWART; SM00212; UBCc; 1.
FROSITE; PS00183; UBIODITIN_CONJUGAT_1; 1.
FROSITE; PS00127; UBIODITIN_CONJUGAT_2; 1.
Ubl conjugation pathway; Ligase; Multigene family.
BINDING 145 145

A -> E (IN REF. 2).

A -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 PALTISKVLLSICSLLTDCNPADPLVGSIATQYLTNRAE 193
                                                                                                                                                                                                                                                                                                                                                                              Score 129.5; DB 1;
Pred. No. 0.17;
34; Mismatches 93;
Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Simil
Matches 53; C
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TIGR; MT2905; -
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Best Local
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                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            1130 QSPRTVGKRQKGGPGPG---GPGPGPGPGPGPGPGPGPGPGPGPGP-----ELICSQQLSGTQR 1180
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hockey E.,
Fleischmann Y.D., Hockey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Härris D., Gordon S.V., Eiglandeir K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Selston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                 2 QQPQPQGQQQ----PGPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLESIFHRGHER
                                                                                                                                                                                                                                                                                                                    Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              itted (APR-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: One of the essential components for the initiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
segregation (By similarity).
-!- TISSUE SPECIFICITY: Testis-specific.
-!- SIMILARITY: Belongs to the SCC3 family.
-!- SIMILARITY: Contains 1 SCD (stromalin conservative) domain.
                                                                                                                                                                                                                                                                                        Length 1256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                  EMBL; AY027880; AAK13052.1; -.
InterPro; IPR005032; STAG.
Pfam; PF03365; STAG; 1.
Meiosis; Cell cycle; Chromosome partition; Nuclear protein.
                                                                                                                                                                                                                                                           1256 AA; 141950 MW; 1C0B3F49D4B8B85D CRC64;
                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT1613:
90 AA.
10-MAY-2000 (Rel. 39, Created)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                        Query Match 5.6%; Score 125.5; Dest Local Similarity 37.2%; Pred. No. 3.3; Matches 32; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFB OR RV2839C OR MT2905 OR MTCY16B7.03.
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Submitted (APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LVVA 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AVSGSVQATDRLM-----KELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 ------GGAAGAFGRPG-GAPRREKSKROKROEYDSMQAP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GEDEG-GEEDLQVRPPVVTVMGHVDHGKTRLLDTIRKANVREAEAGGITQH 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
protein synthesis. Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30s ribosomal subunits. Also involved in the hydrolysis of GTP during the formation of the 70s ribosomal complex (By similarity). SUBCELDULAR LOCATION: CYtoplasmic. SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 POPOGOO-OPGPGO-----QLGGQGAAPGAG--GGPGGGPGPGPCLRRELKLLESIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 HLKRIISDLCKLYNLPQHPDVEMLDQPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 165; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 PRPGGRPGAPGAGRSDAGGGNYRGGGVGAAPGTGFRGRPGGGGGGRPGQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 HRGHERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 IGAYOVAVDLDGSQRLITFIDTPGHEAFTAMRARGAKATDIAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY.
F1B2F3C8A86952C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0315; ELONGATNFCT.
PRINTS; PRO0449; RAGENBSFRANG.
PRODOM; PD186100; IF2; 1.
TIGRPAMS; TIGR00487; IF-2; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS01176; IF2; FALSE_NEG.
Initiation factor; Protein blosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%; Score 123.5; DB 1; 20.5%; Pred. No. 2.8; tive 63; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001806; Ras_trnsfrmng
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000795; EF_GTPbind InterPro; IPR004161; EFTU_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007115; AAK47231.1; -. PIR; B70694; B70694.
HSSP; P13551; IDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94040 MW;
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InterPro; IPR006847; IF2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z81331; CAB03670.1;
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455
509
250
900 AA;
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                   DQDSALHNDLQILKEKEGADF-ILLNFSFKDNFPFDPPFVRVVSPVLSGGYV---LGGGGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kirby R.J.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUIIN TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALITIC ACTIVITY: ATP + ubiquitin + protein lysine - AMP + diphosphate + protein N-ubiquityllysine.
-i- PATHWAY: Ubiquitin conjugation; second step.
-i- MISCELLANEOUS: A cysteine residue is required for ubiquitin-thiolester formation (By similarity).
-i- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
SIRONGEST, TO YEAST UBC1.
-i- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 199;
                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubiquitin-conjugating enzyme E2-22 kDa (EC 6.3.2.19)
(Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 . 92 UBIQUITIN (BY SIMILARITY).
199 AA; 22391 MW; 720CA9595FC0C08F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubl conjugation pathway; Ligase; Multigene family.
                                                                                                                                                                                     199 AA.
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PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 123; DB
llarity 23.0%; Pred. No. 0.4;
Conservative 31; Mismatches
                                                                                  350 ICMELLTKQGWSSAYSIESVIMQISATL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00627; UBA; 1.
Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0015321; UbcD4.
InterPro; IPR000449; UBA_domain.
InterPro; IPR000608; UBQ_conjugat.
                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X92838; CAA63424.1; -. HSSP; P15731; 1QCQ.
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000461; UBQ_cc
SMART; SM00165; UBA; 1.
SMART; SM00212; UBCc; 1
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es 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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P52486;
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Matches
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                                                                   312 ADFILLNFSFKDNFPFPPFPVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIM 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang F., Basavappa R.;

"Crystal structure of the cyclin-specific ubiquitin-conjugating enzyme from clam, E2-C, at 2. O. A resolution.";

Biochemistry 38:6471-6478(1999).

-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROMOTING COMPLEX (APC) AND IS ESSENTIAL FOR THE TRANSITION FROM METAPHASE TO ANAPHASE IN MITOSIS. INVOLVED IN BOTH, DECRADATION OF PROTEINS RESPONSIBLE FOR MAINTAINING SISTER CHROMATID COHESION AT THE ENERT OF ANAPHASE AND OF MITOTIC CYCLINS A AND B AT THE EXIT
5 AVSRIKREFKEVMRSEEIVQCSIKIELVNGQLTELRGEIAGPPD------TPYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "E2-C, a cyclin-selective ubiquitin carrier protein required for the destruction of mitotic cyclins.";
Proc. Natl. Acad. Sci. U.S.A. 93:4294-4299(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family. STRONGEST, TO YEAST UBC11.
                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 42, Last annotation update)
Ubduitin-conjugating enzyme E2-C (EC 6.3.2.19) (Ubiquitin-protein
11gase) (Ubiquitin carrier protein).
Spisula solidissima (Atlantic surf-clam).
Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Townsley F.M., Aristarkhov A., Beck S., Hershko A., Ruderman J.V.; "Domlnant-negative cyclin-selective ubiquitin carrier protein E2-C/UbcH10 blocks cells in metaphase."; Proc. Natl. Acad. Sci. U.S.A. 94:2362-2367(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP + diphosphate + protein N-ubiquityllysine.
-!- PATHWAY: Ubiquitin conjugation; second step.
-!- MISCELLANEOUS: A cysteine residue is required for ubiquitin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-96210635; PubMed-8633058;
Aristarkhov A., Eytan E., Moghe A., Admon A., Hershko A.,
                                                                                                                            372 QISATLVKGK-----ARVQFGANKSQYSL 395
                                                                                                                                                                    112 SLQALLAAAEPDDPQDAVVAYQF---KDKYDL 140
                                                                                                                                                                                                                                                                                   177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-99280704; Pubmed-10350465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 2E2C; 06-APR-99.
InterPro; IPR000608; UBO_conjugat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS OF CYS-114.
MEDLINE-97225958; Pubmed-9122200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mactroidea; Mactridae; Spisula.
NCBI_TaxID=6584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U52949; AAB06237.1; -.
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                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00179; UQ_con; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ATLDGPKDTVYES----LKYK------LTLEFPSDYPYKPPVVKFTTPCWHPN-VDQSG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 KKNQRQDYLNGAVSGSVQATDRLMKELRDIYRS-----QSFKGGNYAVELVNDSLYDWNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 AICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                          C->S: INHIBITION OF CYCLIN B DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE-98090460; PubMed-9427751;
Bohmert K., Camus I., Bellini C., Bouchez D., Caboche M., Benning
                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 177;
SMART; SM00212; UBQ_conjugat; 1.

PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.

PROSITE; PS50187; UBIQUITIN_CONJUGAT_2; 1.

Ubl conjugation pathway; Ligase; Multigene family; Mitosis; Cell cycle; Cell division; 3D-structure.

MUTAGEN 114 114 UBIOTITINE.
                                                                                                                                                                                                                                                                                                                                                                                     70; Indels
                                                                                                                                                                                                                                                                                                                                              06A454E798EE4F3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.5%; Score 122.5; DE Best Local Similarity 24.6%; Pred. No. 0.37; Matches 45; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1048 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Argonaute protein.
AGO1 OR ATIG48410 OR F11A17.3.
                                                                                                                                                                                                                                                                                                                                              20134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                     45
49
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159
177 AA;
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004379;
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MEDLINE—21016719; PubMed—11130712;

MEDLINE—21016719; PubMed—11130712;

MEDLINE—21016719; PubMed—11130712;

MEDLINE—21016719; PubMed—11130712;

MINTEO O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,

Munch S., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dowar R.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dowar R.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Treng B., Hulzer J.L., Jehlung T.V., Feng J.-D., Fong B., Hulzer J.L., Jehlung B., Hunter J.L., Jehlung J., Johnson-Hopson C., Khan S., Khaykin E.,

A kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.P.,

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Militscher J., Maranda M., Nguyen M., Ngoney T., Rowley D.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tanlon L.J., Tambunga G., Toriumi M.J., Town C.D.,

A Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED distraction the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 PPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRI------ISDLCKLYNL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- 109
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1048;
defines a novel locus of Arabidopsis controlling leaf
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116190 MW; 3E5146343A09C541 CRC64;
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Pred. No. 3.9;
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InterPro; IPR003100; PAZ.
InterPro; IPR003165; Piwi.
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                   development.";
EMBO J. 17:170-180(1998).
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Pfam; PF02171; Piwi; 1.
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Matches 87; Conserv
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A MEDINE-22388557; Pubmed-12477932;

A KIBSULE-22388557; Pubmed-12477932;

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,

B Stapleton M., Soares M.B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Tahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Milting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                 ----VNRAVMKQLVDNYRDSHLGSRLPAYDGR------KSLYTAGPLPFNSKEFR 268
                                                                                                                                                                                                                              POHPDVEMLDOPLPAEQCTQEDVSSEDEDEEMPEDTEDLDHYE--MKEEEPAEGKKSEDD 220
                                                                                                                                                                                                276 VELVNDSL-----YDWNVKL-----LKVDQDSALHNDLQILKEKEGAD 313
                                                                                                                                                                                                                                                                                      314 FILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAY-SIESVIMQ 372
                                                                                                                                                                                                                                                                                                                              323 IVLRELPISRYIPVGRSF---YSPDIGKKQSLGDGL-----ESWRGFYQSIRPTQMG 371
                                                                     180 PMRP-----GKGQSGKRCI---VKANHFFAELPD--KDLHHYDVTITPEVTSRG-----
                                                                                                                221 GIGKENLAILEKIKKNORODYLNG---AVSGSVQATDRLMKELRDIYRS--OSFKGGNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
PROTEINS. MEDIATES THE SELECTIVE DEGRADATION OF SHORT-LIVED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ublquitth-conjugating enzyme E2 E1 (EC 6.3.2.19) (Ubiquitin-protein ligase E1) (Ubiquitin carrier protein E1) (UbcH6).
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STRAIN-BALDA/C; ITSUE-Brain;

MEDILINE-96162026; Pubmed-8576556;

Matuschewski K., Hauser H.P., Treier M., Jentsch S.;

Tidentification of a novel family of ubiquitin-conjugating enzymes with distinct amino-terminal extensions.";

J. Biol. Chem. 271:2789-2794 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine - AMP + diphosphate + protein N-ubiquityllysine.
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                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 SEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNORODYLNGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 SGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RIQKELADITLDPP---PNCSAGPKGDNIYEWRSTIL--GPPGSVY----
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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Catarrhini; Hominidae; Homo.
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MARRY; SM00212; UBCc; 1.
PROSITE; PS00183; UBICUITIN_CONJUGAT_1; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
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J. Biol. Chem. 276:38966-38970(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X92665; CAA63353.1; -.
EMBL; EC003781; AAH03781.1; -.
HASP; P15731; 10C0.
MGD; MGI:107411; Ube2e1.
InterPro; IPR000608; UBQ_conjugat.
Pfam; PF00179; UQ_con; I.
ProDom; PD000461; UBQ_conjugat; 1.
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MEDLINE-21486406; Pubmed-11481332;
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KIAA0665.
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Human).
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SEQUENCE FROM N.A.
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SEQUENCE
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 EDFIQ-----FATVYGAEQVKDLTKYLDPSGLGVISFEDFYQGITAIRNGDPDGQCYGGV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 PRGSV----PGDPVRIHCNITESYPAVP--PIWSVESDDPNLAAVLERLVDIKKGNTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 LQHLKRIISDLCKLYNLPQHPDVEMLDQPL-------PAEQCTQED
                                                                       "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                      "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
                                                                                                                                                                                                    Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                    Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                   Wallis J., Lloyd C., Hall R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-1- SUBUNIT: Binds to RAB11 and RAB25.
-1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 120; DB 1; Length 75 23.8%; Pred. No. 3.7; ive 28; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
264CEC399F28AFB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQPQGQQQPGPGQQLGG - - - - QGAAPGAGGGP - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0017137; F:RAB interactor activity; NAS. InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-21096910; PubMed=11157797;
                   MEDLINE-98403880; PubMed-9734811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB014565; BAA31640.1; --
EMBL, AE006463; AAK61232.1; --
EMBL, ALO13881; CAC192745.1; --
EMBL, AL049542; CAC17519.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF395731; AAL12940.1; -.
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PIR; T00367; T00367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00036; efhand; 2.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding; Repeat.
CA_BIND 215 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             756 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
rissum-Brain;
                                                                                                                                                                                                                                           D.R.;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 132-917 FROM N.A. (ISOFORM A).
MEDLINE-20237674; PubMed-10773462;
Slavov D., Hattori M., Sakaki Y., Rosenthal A., Shimizu N.,
Minoshima S., Kudoh J., Yaspo M., Ramser J., Reinhardt R., Reimer C.,
Clancy K., Rynditch A., Gardiner K.;
"Criteria for gene identification and features of genome organization:
analysis of 6.5 Mb of DNA sequence from human chromosome 21.";
Gene 247:215-232(2000).
                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain, Heart, Kidney, Lung, Muscle, Placenta, and Testis;
Chapot-Skovsgaard F.M., Guipponi M., Lyle R., Antonarakis S.E.;
"Isolation and initial characterization of a putative human chromosome
                                                                                                                                                                                                                                                                                          "From PREDs and open reading frames to cDNA isolation: revisiting the human chromosome 21 transcription map."; Genomics 78:46-54(2001).
                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chapot F.,
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               21 transcription factor.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
MEDLINE-21564202; Pubmed-11707072;
Reymond A., Friedli M., Neergaard Henrichsen C., Chapot Deutsch S., Ucla C., Rossier C., Lyle R., Guipponi M., Antonarakis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId-Q9Y5B6-3; Sequence-VSP_004263, VSP_004264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoId=Q9Y5B6-4; Sequence=VSP_004265, VSP_004266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms-4;
GCFC_HUMAN STANDARD; PRT; 917 AA. 0975B6; G9NYOO; 10-MAY-2000 (Rel. 39, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-EFS-2003 (Rel. 42, Last annotation update) 6C-Tich sequence DNA-binding factor homolog. GCFC OR C21ORF66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 489-815 FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId-Q9Y5B6-2; Sequence-VSP_004267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId-Q9Y5B6-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Ubiquitous. SIMILARITY: TO GCF/TCF9.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY033903; AAK68721.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK68724
                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                           NCBI_TaxID=9606;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                             /FTId-vSP_004265.
Missing (in 1soform D).
/FTId-vSP_004266.
LIGNFLQWYGIFSNKTLQELSIDGLLNRYILMAFQNSEYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSIKKAONVINCFPKOWFMNLKGERTISOLENFCRYLVHLA
DTIYRNSIGCSDVEKRNARENIKQIVKLLASVRALDHAMSV
ASDHNVKEFKSLIEGK -> VIKPPFQRGSCPIPRRKECCS
ERPRRIWTDRPCVVFS (in isoform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCNITESYPAVPPIWSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 -LDQPLP----AEQCTQED--VSSEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 KENLAILEKIKKNORODYLNGAVSGSVOATDRIMKELRDIYRSOSFKG-GNYAVELVNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 SNALSSLNVLRPGEIPD---ÀAFIHAARKKRQMARELGDFTPHDNEPGKGRLVREDENDA
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15-SEP-2003 (Rel.:42, Last annotation update)
Ubiquitin-conjugating enzyme E2 E1 (EC 6.3.2.19) (Ubiquitin-protein UBase E1) (Ubiquitin carrier protein E1) (UbcH6).
                     Genew; HGNC:13579; C21orf66.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0000577; F:DNA binding activity; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                    NKALMAPN -> SQSILKTK (in isoform D)
                                                                                                                                                                                                                    SVQFRKLL (in isoform C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches 115; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 EQEPPPLLPPPGTGEEAGPGGGDRAPGGESLLGPGPSP-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 LYDWNVKLLKVDQDSALHNDLQILKEK------EGAD 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_004267.
MISSING (IN REF. 4).
7; 855960A1D50A7789 CRC64;
                                                                                                                                                                                                                                          /FTId=VSP_004263.
Missing (in isoform C).
/FTId=VSP_004264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 120; 23.3%; Pred. No. 4
                                                                                                                                                                                                                 VPLINELE
EMBL; AF153208; AAD34617.1; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 711 MI:
917 AA; 104803 MW;
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                                                                                                                                                                                     Alternative splicing.
VARSPLIC 462 46
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Best Local Similarity
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P51965;
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                                                                                                                                       **X TEASURE—COLODA;

**X MEDLINE—22388257; PubMed=124,7932;

**X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**X Attashar R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Boraldo M.F., Casvant T.L., Scheetz T.E.,

**A Stapleton M. J. Osdares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

**A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

**A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Rilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**A Hutterfield Y.S.N., Krzywinski M.I., Skalska W.,

**A Butterfield Y.S.N., Krzywinski M.I., Skalska W.,

**Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

**Cheneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 SEDEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 SGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQIL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SDDDSRASTSSSSSSSNQQTEKETNTPKKKESKVSMSKNSKLLSTSAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family. STRONGEST, TO DROSOPHILA UBCD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences.";
Proc. natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO PROTEINS. MEDIATES THE SELECTIVE DEGRADATION OF SHORT-LIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for ubiquitin-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP diphosphate + protein N-ubiquityllysine.
-!- PATHRAX: Ubiquitin conjugation; second step.
-!- SUBGNIT: INPERACTS WITH RNF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO: GO:0004840; F:ubiquitin conjugating enzyme activity; GO: GO:0004842; F:ubiquitin-protein ligase activity; TAS. Interpro: IPR000608; UBQ_conjugat.
Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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-i- MISCELLANEOUS: A cysteine residue is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ubl conjugation pathway; Ligase; Multigene family. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%; Pred. No. 0.64; ive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00183; UBIQUITIN_CONJUGAT_1; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 119.5;
Biol. Chem. 271:2795-2800(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 AA; 21404 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X92963; CAA63539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC009139; AAH09139.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:12477; UBE2E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thiolester formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABNORMAL PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
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Best Local Simil
Matches 49; (
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KEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSI 366
                   91
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WEDLINE-22388257; Pubmed-12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pranney C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Hirakawa M., Yamaguchi H., Imai K., Shimada J., Shiina S., Tamiya G., Oka A., Inoko H.; "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A. (ISOFORM 1), ALTERNATIVE SPLICING (ISOFORM 2), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY.
MEDLINE-2154388; PubMed=11707778;
Brown S.E., Campbell R.D., Sanderson C.M.;
Novel NG36/G9a gene products encoded within the human and mouse MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P.,
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.,
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Salivary gland;
Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sudiyama T., Tite R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma I
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               BAT8_HUMAN STANDARD; 09600; 0900L8; 09x331; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Histone-lysine N-methyltransferase, H3 lysine-9 specific 3 (EC 2.11.143) (Histone-H3*K9 methyltransferase 3) (H3*C 2.11.143) (Histone-H3*K9 methyltransferase 3) (H3*C 2.11.143) (Histone-H3*K9 methyltransferase 3) (H3*C 2.11.143) (H3*C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   ESVIMOISATLVK-GKARVQFGANKSQYSLTRAQ 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome 12:916-924(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAT8 OR G9A OR NG36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                         307
                                                                                                                                                     92
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                             21
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-:- SIMILARITY: Contains 7 ANK repeats.
-:- SIMILARITY: Contains 1 pre-SET domain.
-:- SIMILARITY: Contains 1 pre-SET domain.
-:- SIMILARITY: Contains 1 bost-SET domain.
-:- SIMILARITY: Contains 1 bost-SET domain.
-:- CADTION: NG36 and 69a were originally thought to derive from two separate genes. Ref.3 shows that all G9A transcripts also contain the in frame coding sequence of NG36.
-:- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to erroneous gene model prediction.
-:- CAUTION: It is not known whether Met-1 or Met-21 is the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION IN COMPLEX WITH E2F6; TFDP1; MAX; MGA; EUHMTASE1; CBX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylated histones. Probably trecruiting HP1 proteins to methylated histones. Probably targeted to histone H3 by different bna-binding proteins like E2F6, MGA, MAX and/or DP1. Also methylates histone H1 (By similarity).

CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine = sudenosyl-L-monecysteine + histone N6()-methyl-L-lysine.

SUBUNIT: Part of the E2F6.com-l complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: Histone methyltransferase. Preferentially methylates Lys-9 of histone H3 and Lys-27 of histone H3 (in vitro). H3 Lys-9 methylation represents a specific tag for epigenetic
Richards S., Worley K.C., Hale S., Garcia A.M., Gay.L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youchman A., Young A.C., Shevchenko Y., Budfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U.; Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isold-096KQ7-1; Sequence-Displayed;
Name=2; Synonyms-NG36G9a-SPI;
Isold-096KQ7-2; Sequence-VSP_002211;
Name=3; Synonyms-NG36;
Isold-096KQ7-3; Sequence-VSP_002212, VSP_002213;
ISOG-096KQ7-3; Sequence-VSP_002212, VSP_002213;
TISSUE SPECIFICITY: Expressed in all tissues examined, with high levels in fetal liver, thymus, lymph node, spleen and peripheral blood leukocytes and lower level in bone marrow.
SIMILARITY: BELONGS TO THE HISTONE-LYSINE METHYLITRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2126082; PubMed-11316813;
Tachlbana M., Sugimoto K., Fukushima T., Shinkai Y.;
"Set domain-containing protein, 69a, is a novel lysine-preferring mammalian histone methyltransferase with hyperactivity and specific 3. Biol. Chem. 276:25309-25317(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RING1; RNF2; MBLR; L3MBTL2 AND YAF2.
MEDLINE-21999559; PubMed-12004135;
Ogawa H., Ishiguro K.-I., Gaubatz S., Livingston D.M., Nakatani Y.;
"A complex with chromatin modifiers that occupies E2F- and
Myc-responsive genes in GQ cells.";
Science 296:1132-1136(2002).
                                                                                                                                                                                                                                                                                                                                                                               gene in the human major histocompatibility complex encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regions. Does not associate with heterochromatin.
                                                                                                                                                                                                                                                                                     SEQUENCE OF 195-1210 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                       novel protein containing ankyrin-like repeats.";
Blochem. J. 290:811-818(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYMATIC ACTIVITY, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L3MBTL2 and YAF2.
SUBCELLULAR LOCATION: Nuclear;
                                                                                                                                                                                                                                                                                                                                   MEDLINE-93207535; Pubmed-8457211;
Milner C.M., Campbell R.D.;
                                                                                                                                                                                                                   human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                           TISSUE-Histiocytic lymphoma;
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                                                                                                                                                                                                                                                                                                                                                                                 "The
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134

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135 L------VDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEM 170
                                                                                                                                                                                     283 VDSDSKSEVEALTEQLSEEEEEEEEEEEEEEEEEEEEEEEEEEEE
                                                                                                      171 LDQPLPAE-QCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEEPAE-GKKSEDDGIGKENLA 228
                                     -----GHATKSFPSSPSKGGSCPSRAKMSMTGAGKSPPSVQSLAMRLLSMPGAQGAAAA 163
                                                                                 ---WSVESDDPNLAAVLER
    ---GAGAGAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker K., Pak M., Salkoff L.;
an extended gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Butler A., Wei A.G., Salkoff L.;
"Shal, Shab, and Shaw: three genes encoding potassium channels in
Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hegde P., Gu G.G., Chen D., Free S.J., Singh S.; "Mutational analysis of the Shab-encoded delayed rectifier K(+) channels in Drosophila."; J. Biol. Chem. 274:22109-22113(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Oregon-R;
MEDINE-89146139; Pubwed-2493160;
Butler A., Weil A.G., Baker K., Salkoff L.;
"A family of putuative potassium channel genes in Drosophila.";
Science 243:943-947(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIKE_DROME STANDARD; PRT; 985 AA.

P17370, 076805; 0917T9; 0917U0;
01-NOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation shab.
28-FEB-2003 (Rel. 41, Last annotation update)
Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM SHORT), AND MUTAGENESIS
                                                                               GPHLPPRGSVPGDPVRIH-CNITESYP--AVPPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
ESIFHRGHERFRIASACLDELSC----EFLLAGAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 18:2173-2174(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wel A.G., Covarrubias M., Butler A.,
"K+ current diversity is produced by
conserved in Drosophila and mouse.";
Science 248:599-603(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM LONG). MEDLINE-90245668; PubMed-2336395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Canton-S;
MEDLINE-99348357; PubMed=10419540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM LONG)
MEDLINE-90239553; Pubmed-2333511;
                                                                                                                                                                                                                                                                                                                      229 ILEKIKKNQRQD 240
                                                                                                                                                                                                                                                                                                                                               | || || |:|
340 --RKAKKKWRKD 349
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 6.
SMART; SM00018; PRESET; 1.
SMART; SM00117; SET; 1.
PROSITE; PS50088; ANK_REPEAT; 5.
PROSITE; PS5086; PRE_SET; FALSE_NEG.
PROSITE; PS50867; PRE_SET; FALSE_NEG.
PROSITE; PS50867; PRE_SET; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; Score 118.5; DB 1; Length 1210;
3.4%; Pred. No. 8.5;
ve 34; Mismatches 120; Indels 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPVPEKRP -> VSGMGEMG (in isoform 3)
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A -> Q (IN REF. 5; AAH18718).
A -> G (IN REF. 5; AAH10970).
N -> T (IN REF. 1 AND 4).
PP -> TR (IN REF. 2; AAH02686).
P -> S (IN REF. 3).
C -> R (IN REF. 3).
C -> R (IN REF. 5).
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Missing (in isoform 3).
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DOMAIN 2 13 POLY-ALA.
DOMAIN 160 163 POLY-ALA.
DOMAIN 300 326 POLY-GLU.
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ANK 5.
ANK 6.
ANK 7.
                                                                                                                                                                                                                                                                                           EMBL; BC002686; AAH02686.1; ALT_INIT.
EMBL; BC018718; AAH18718.1; ALT_INIT.
EMBL; BC020970; AAH20970.1; ALT_INIT.
EMBL; X68938; CAA49491.1; ALT_INIT.
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                                                                                                                                                                    EMBL; AF134726; AAD21811.1; ALT_SEQ.
EMBL; AF34726; AAD21812.1; ALT_SEQ.
EMBL; AP000502; BAB623294.1; ALT_SEQ.
EMBL; AP000502; BAB62295.1; ALT_SEQ.
EMBL; AJ315532; CAC86666.1;
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InterPro; IPR002110; ANK
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InterPro; IPR003606; Zn2
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178
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Pfam; PF00856; SET; 1.
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1994
1210 AA;
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Ann K.H., Doyle C., Baxter E.G. Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andraws-Frankoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktarodlu L., Beasley E.M.,

Rabeson K.Y. Benos P.V., Bernan B.P., Blandari D., Bolshakov S.,

Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

Raboson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Raboson K., Doup L.E., Downes M., Dugan-Rocha S., Plaischman W.,

RA Bortis M.J., Evangalista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Glodek A., Gong F., Gorrell J.H. G. Gelbart W.M., Classer K.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hell M.-H., Ibegam C.J., A.

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison D.L.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin Z.,

Liu X., Mattel B., McIntosh T.C., McLeod M.P., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

Rabazzolo M., Pittuano G.S., Pan S., Pollard J., Woshrefi A.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

Millams S.M., Wooden F.N., Simpson M., Stupski M.P., Smith H.O.,

Albert K.M., Where R. Wolley K.C., Wu D., Yang S., Yao Q. A.,

R. Schenc 287. 23veri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,

Schenc 287. 23veri J.S., Zhan M., Vannay B., Wang C., Yu R., Schen E.C., Stan M., Wooder C., Wassenbach J.,

Millams S.M., Wooden W.D., Weissenbach J.,

R. Schenc 287. 23veri J.S., Zhan M., Shun B., Zhu X., Smith H.O.,

Schenc 287. 23veri J.S., Zhan M., Weissenbach J.,

R. Schenc 287. 23veri J.S., Zhan M., Shun B., Shun B., Shun B., Shun B., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-Short;
Isold-P17970-2; Sequence-VSP_000960;
Isold-P17970-2; Sequence-VSP_000960;
DDVALN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

TO SPECIFIC SUBCELLULAR COMPARTMENTS.

MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVERY THIRD POSITION. SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. SHAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Long;
IsoId=P17970-1; Sequence=Displayed;
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(See http://www.lsb-sib.ch/announce/ sequence differs from that shown due to erroneous entities requires a license agreement (St or send an email to license@isb-sib.ch). gene model prediction.

AF084525; AAC33365.1; -. AE003476; AAC22232.1; ALT\_SEQ. AE003476; AAG22233.1; ALT\_INIT. EMBL; M32659; AAA28896.1; EMBL;

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214 SQQIVGSVGGVGVGASSQSI--SGGVPTHSQSNTTGALQRTHSRSMSSIPPPEPFMIAQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 CEFLLAGAGGAGAAPGPHLPPRGSVP-----GDPVRIHCNITESYPAVPPIWSVE 122
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LQNQRMDNLEQDVPVEFECCFCTTKGLPGCHGECIPLRANS
                                                                                                                                                                                                                                                                                                                                                 SMART; SM00225; BTB; 1.
Transport; Ion transport; Ionic channel; Voltage-gated channel;
Potassium channel; Potassium transport; Potassium; Transmembrane;
Glycoprotein; Phosphorylation; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; . Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> VMEMGAVSMTTTFPRPRDCPSR (IN REF. 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY PKA) (POTENTIAL)
PHOSPHORYLATION (BY PKA) (POTENTIAL)
PHOSPHORYLATION (BY PKA) (POTENTIAL)
MISSING (In 1800 form Short).
FTIGH-VSP_000960.
R->O: IN ALLELE SHAB-1; TEMPERATURE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V->D: IN ALLELE SHAB-1; TEMPERATURE-
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N REF. 1, 2 AND 3).
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S -> G (IN REF. 1, 2 AND 3).
R -> G (IN REF. 1, 2 AND 3).
S -> G (IN REF. 1, 2 AND 3).
FS -> CA (IN REF. 1, 2 AND 3).
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27; Mismatches 102; Indels
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A -> S (IN REF. 1, 2 AND 3).
V -> I (IN REF. 5).
C -> T (IN REF. 5).
C -> Y (IN REF. 5).
V -> I (IN REF. 5).
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106359 MW; 59E38AD35F064AC8 CRC64;
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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N-LINKED (GLCNAC.
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                                  FIGURES: FBGN0003183; Shab.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR00821; Ion_trans.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003091; K_channel.
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                                                                                                                                               Interpro; IPR003131; K_tetra.
Interpro; IPR003971; Kv9_channel.
Interpro; IPR003968; Kv_channel.
Interpro; IPR005820; M+channel_nlg.
Pfam; PF00520; Ion_trans; 1.
Pfam; PF005214; K_tetra; 1.
                                                                                                                                                                                                                                                                              PRINTS; PRO169; CCHANNEL.
PRINTS; PRO1494; KV9CHANNEL.
PRINTS; PRO1491; KVCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 5.3%;
1 Similarity 23.5%;
63; Conservative 2'
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796
717
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TRANSMEM 43
TRANSMEM 47.
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Best Local S:
Matches 63,
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                     272 SKAVNSRVSINVGGVRHEVLWRTLERLPHTRLGRLRECTTHEAIV-ELCDDYSLADNEYF 330
                                                                      ---LAAVLERLVDIKKGNTLLLQHLKRIISDLCKLYNL----- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 GTI-----DGAVGTVYEDLRYK-----LSLEFPSGYPYNAPTVKFVTPCFHPN-VDSH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AILEKIKKNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVNDSLYDWN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 VKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 GAICMELLTKQGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thiolester formation (By similarity).
--- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
SIRRONGEST, TO YEAST UBC11.
HSSP, 095044; 2E2C.
InterPro; IPRO00608; UBO_conjugat.
Pfam; PF00179; UQ_con; 1.
Probom; PD000461; UBO_conjugat; 1.
                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinee; Xenopus
                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ubfquitin-conjugating enzyme X (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
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Whosite; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ubl conjugation pathway; Ligase; Multigene family; Mitosis; Cell cycle; Cell division.
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25.0%; Pred. No. 0.77;
tive 36; Mismatches 79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 63-80 AND 99-108 MEDLINE-96298869; Pubmed-8723350;
                                                                                                                                                                                                         PRT; 179 AA
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                                                        ---DVEMLDO---
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Best Local Similarity 25.0%
Matches 46; Conservative
                                                                                                                                                                                                         STANDARD;
SDDPN-----
                                                     163 -PQHP-----
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123
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completed: July 29, 2003, 13:45:22
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166 LHEQ 169
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Job time :
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408 IHEK 411

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2003, 13:44:59; Search time 30 Seconds

(without alignments)
595.173 Million cell updates/sec

Title: US-10-005-549-2
Sequence: 1 MOOPOPOGOQOPGPGQQLGG.......KSLVQIHEKNGWYTPPKEDG 422
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/packfiles1.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Appii Appii Appii Appii Appii Appii Appii Appii Sequence 5, Description Sequence ednence sequence -09-318-317-3 -09-196-525-1 Match Length DB Query 135.5 135.5 135.5 122.5 122.5 120.5 120.5 119.5 118.5 Result è. 

Sequence 65, Appl Sequence 77, Appl Sequence 73, Appl Sequence 6, Appl Sequence 8, Appl Sequence 2, Appl Sequence 4, Appl Sequence 5, Appl Sequence 5, Appl Sequence 7, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 22, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl S	
US-09-535-008-65 US-09-535-008-73 US-09-535-008-73 US-08-464-604A-6 US-08-828-533-8 US-09-772-156-8 US-09-132-861-4 US-09-132-861-4 US-09-252-991A-24114 US-09-252-991A-24114 US-08-46-604A-7 US-08-56-419-23 US-08-556-419-23 US-08-556-419-23 US-09-394-272-9 US-09-394-272-9	ALIGNMENTS
4440040000400000441	
1679 1681 1682 193 177 177 177 140 907 448 147 147 1684 1084	
115.5 1115.5 1113.5 1112.5 1112.5 1111.5 111	
00000000000000000000000000000000000000	

Indels 59; Gaps GENERAL INFORMATION:
APPLICANT: A1-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING ENZYME Length 295; Ouery Match
6.1%; Score 135.5; DB 2;
Best Local Similarity 21.4%; Pred. No. 0.0012;
Matches 42; Conservative 33; Mismatches 62; Incyte Pharmaceuticals, Inc COMPUTER READALLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PRASTSO VERSION 1.5
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/679,765
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Blilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0093 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 5: Sequence 5, Application US/08679765 Patent No. 5840866 3174 Porter Drive SEQUENCE CHARACTERISTICS: LENGTH: 295 amino acids TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE: STRANDEDNESS: single CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Ph STREET: 3174 Port CITY: Palo Alto STATE: CA COUNTRY: U.S. TYPE: amino acid LIBRARY: GenBank CLONE: 788905 94304 US-08-679-765-5

273 NYAVELVNDS-LYDMNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPF 331

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sequence

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331
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                                --LTRAQOSYKSLVQIHE--- 410
                                                     92
77 FR-FTPAIYHPNVYRDGRLCISILHQSGDPMTDEPDAETWSPVQTVESVLISIVSLLEDP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 NYAVELVNDS-LYDWNVKLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPF
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                                                                                                                                                                                                                 Sequence 5, Application US/09318317
Patent No. 6172199
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLman, Jennifer L.
ATTLE OF INVENTION: ENZYME
TITLE OF INVENTION: ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                   3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0093 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 VRVVSPVLSGGYVLGGGAICMELLTKQG-
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APPLICATION NUMBER: 09/196,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                    ----VKGKARVQFGANKSQYS-
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    Telephone: 415-855-0555
                                                                                                  ----KNGWYTPPKED 421
                                                                                                                                   196 NKDMADNFWYDSDLDD 211
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 amino acids
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94304
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                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Pa.
STATE: CA.
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                                                                                                                                                                                     RESULT 3
US-09-318-317-5
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                                                                                                    411
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                                                                                                                                   136 NINSPANVDAAVDYRKNPEQYRQRVKMEVERSKQDIPKGFIMPTSESAYISQSKLDEPES 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --WSSAYSIESVIMQISATL--- 377
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----GGFFKAQMRFPEDFPFSPPQ 76
                                    --WSSAYSIESVIMOISATL--- 377
   --GGFFKAQMRFPEDFPFSPPQ 76
                                                       ----LTRAQQSYKSLVQIHE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING
TITLE OF INVENTION: ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 135.5; DB 2;
21.4%; Pred. No. 0.0012;
Live 33; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 SFHIELEDDSNIFTWNIGVMVLNEDSIYH----
                                    332 VRVVSPVLSGGYVLGGGAICMELLTKQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
     SFHIELEDDSNIFTWNIGVMVLNEDSIYH---
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APPLICATION NUMBER: US/09/196,525
                                                                                                      ----VKGKARVQFGANKSQYS---
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APPLICATION NUMBER: 08/679,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09196525
Patent No. 5989883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                      Goli, Surya K.
Hillman, Jennifer
                                                                                                                                                                      411 -----KNGWYTPPKED 421
                                                                                                                                                                                                     196 NKDMADNFWYDSDLDD 211
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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LIBRARY: Generate 788905
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                                                                                                                                                                                                                                                                   -09-196-525-5
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349 AICMELLTKOGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQOSYKSLVQI 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 QKERPRDMTTSKERHSV--SKRLQQELRTLLMSGDPGITAFPDG------DNLFKW-V 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 KKNQRQDYLNGAVSGSVQATDRLMKELRDIYRS-----QSFKGGNYAVELVNDSLYDWNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 KLLKYDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu, Hongtao
TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 122.5; DB 3;
Pred. No. 0.0076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner Ph.D., Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HAZ-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kirschner, Marc W.
Townsley, Fiona
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                 31-MAR-1997
                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617)526-6000
TELEFRAX: (617)526-6000
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: linear
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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HEK 169
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136 NINSPANVDAAVDYRKNPEQYKQRVKMEVERSKQDIPKGFIMPTSESAYISQSKLDEPES 195
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                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tyers, Mike
APPLICANT: Tyers, Mike
APPLICANT: Wildens, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.100501
CURRENT APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1999-07-10
PRIOR FILING DATE: 1997-10-24.
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 FR-FTPAIYHPNVYRDGRLCISILHQSGDPMTDEPDAETWSPVQTVESVLISIVSLLEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aristarkov, Alexander
APPLICANT: Aristarkov, Alexander
APPLICANT: Yu, Hongrao
APPLICANT: Yu, Hongrao
TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.1%; Score 135.5; DB
Best Local Similarity 21.4%; Pred. No. 0.0012;
Matches 42; Conservative 33; Mismatches 6
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                                                                                                                                                                                       Sequence 22, Application US/09177165A
Patent No. 6426205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae US-09-177-165A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08828533 Patent No. 6180379
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60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Kirschner, Marc W. : Townsley, Fiona
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                                       411 ----KNGWYTPPKED 421
                                                                                196 NKDMADNFWYDSDLDD 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3.
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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California
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                                                        TELEPHONE:
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US-08-785-190-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 KKNQRQDYLNGAVSGSVQATDRLMKELRDIYRS-----QSFKGGNYAVELVNDSLYDWNV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ATLDGPKDTVYES----LKYK-----LTLEFPSDYPYKPPVVKFTTPCWHPN-VDQSG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AICMELLTKOGWSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQQSYKSLVQI 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 OKERPRDMITSKERHSV--SKRLQQELRILLMSGDPGITAFPDG------DNLFKW-V 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 KLLKVDQDSALHNDLQILKEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.5%; Score 122.5; DB 4; Length 178; 24.6%; Pred. No. 0.0076; ive 35; Mismatches 70; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LeFebvre, Rance B.
APPLICANT: Derng, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
NUMBER OF INVENTION: Lyme Disease
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                       NAME: Kerner Ph.D., Ann-Louise
REGISTRATION NUMBER: 33,523
REFERRNCE/DOCKET NUMBER: HAZ-015CIP
TELECOMMUNICATION INFORMATION:
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,156
FILING DATE: 31 Mar-1997
CLASSIFICATION: 435
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
FRAGMENT TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                     APPLICATION NUMBER: 08/828,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,589
FILING DATE: 19910628
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                                                                                                                                                                                                                                              TELEPHONE: (617)526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        FILING DATE: 1997-03-31 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/07720589
Patent No. 5324630
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     LENGIH: 178 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPEATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: James M. Heslin
379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.6%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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STATE: California
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| HEK 169
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US-09-772-156-3
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204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 GADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYV----LGGGAICMELLTRQGWS--SAY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIESVIMQISATLVKGKARVQF-----GANKSQYSLTRAQQSYKS----LVQIHEK- 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PVFLEVIDPITNLGTLQLIDLNTG-VSLKESTQQGIQRYGIY
                                                                                                                                                                                                                                                                                                                                                                Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions for Diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATORS TSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                  29,541
R: 2307U-330/UC 90-017-1
                                                                                                                                                                                                                                                                                                                                                             5.4%; Score 120.5; DB 1; 21.3%; Pred. No. 0.085;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08785190; Patent No. 5977339; GENERAL INFORMATION: APPLICANT: LeFebvre, Rance B. APPLICANT: Perng, Guey-Chen TITLE OF INVENTION: Methods and Con TITLE OF INVENTION: Lyme Disease
                                                                                                                                                                                                                                                                                                                                                                                                              62;
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: James M. Heslin
379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 --NGW----YTPPKED 421
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                                                                                                                         TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: AMINO ACID
                                                                                              415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-07:720-589-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. F
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08679765 Patent No. 5840866
                                                                                                                                                                                                                                                                                                                                                                                                  62;
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 21.3%;
Matches 80; Conservative 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                     : 700 amino acids
AMINO ACID
                                                                                                                                                                                                TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920629
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein
PCT-US92-05539-2
                                                                                                                                                                                                                                                                                         linear
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CITY: Pa
STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 EMKEEEPAEGK--KSEDDGIGKENLAI-----LEKIKK-NQRQDYLNGAVSGSVQATDRL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 MK-----ELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::| :|:| :|:| :|-----SKDDKASKDGKALDLDRELNSKASSKEKS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 SIESVIMQISATLVKGKARVQF-----GANKSQYSLTRAQQSYKS----LVQIHEK- 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 GADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYV----LGGGGAICMELLTKQGWS--SAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 SS------PVFLEVIDPITNLGTLQLIDLNTG-VSLKESTQQGIQRYGIY
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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5.4%; Score 120.5; DB 2; Length 700;
Best Local Similarity 21.3%; Pred. No. 0.085;
Matches 80; Conservative 62; Mismatches 133; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LeFebvre, Rance B.
APPLICANT: Perng, Guey-Chen
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: Lyme Disease
                                                                                                                                    2307U-330/UC 90-017-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application PC/TUS9205539
; GENERAL INFORMATION:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/720,589
                                                                                        NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 23(
TELECOMMUNICATION: TELEPHONE: 415-326-2400
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CORRESPONDENCE ADDRESS:
ADDRESSEE: James M. Heslin
STREET: 379 Lytton Avenue
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642 SSNDWRLAKFSPKNLD 657
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           700 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396
                                                                                                                                                                                      415-326-2422
                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-785-190-2
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California
                                                                                                                                                                                                                                                              amino acid
                                                          FILING DATE:
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                                                                                                                                                                                      TELEFAX:
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STATE:
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90 HLPPRGSVPGDPVRIHCNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHL 149
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APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 700;
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-330/UC 90-017-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFRAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                            Score 120.5; DB 5;
Pred. No. 0.085;
2; Mismatches 133;
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204

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FILING DATE: ATTORNEY/AGENT INFORMATION:
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COUNTRY: U.
ZIP: 94304
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                                                                                                                                                                                                                                                                                                      LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ALYONG, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBLOUITIN-CONJUGATING
TITLE OF INVENTION: BNZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 119.5; DB 2;
Pred. No. 0.015;
2; Mismatches 96;
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,765
FILING DATE: Filed Herewith
ATTONNEY, PAGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTARTION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0093 US
TELECOMMUNICATION INFORMATION:
TELECHNONE: 415-855-0555
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FastSEQ Version 1.5
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                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.4%;
Best Local Similarity 22.9%;
Matches 49; Conservative 3
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                                                                                                                                                                                                                                                            LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                        415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GenBank
CLONE: 1064914
                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
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307 KEKEGADFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSI 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SDDDSRASTSSSSSSSSNQQTEKETNTPKKKESKVSMSKNSKLLSTSAK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
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APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Janifer L.
APPLICANT: Hillman, Janifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 119.5; DB 2;
22.9%; Pred. No. 0.015;
tive 32; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 ESVIMQISATLVK-GKARVQFGANKSQYSLTRAQ 399
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                                                 PF-0093 US
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SOFTWARE: FRALSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,317
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Patent No. 6172199
                                                                        **LLEFAX: 415-855-0555

**TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acids
STRANDENNESS: single
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                          36,749
                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 22.9%
Matches 49; Conservative
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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APPLICATION NUMBER: US/09/196,525
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APPLICATION NUMBER: 08/679,765
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-845-4166
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Best Local Similarity 21.1%
Matches 45; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
         STRANDEDNESS: single
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MEDIUM TYPE: Diskett
                                                                              LIBRARY: PGANNOT01
CLONE: 61887
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US-08-679-765-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           247 SGSVQATDRIAKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQIL 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence I, Application US/08679765
Patent No. 5840866
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HIllman, Jennifer L.
APPLICANT: HILlman, Jennifer L.
ANOWER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                               5; DB 3; Length 193; 0.015; hes 96; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 ESVIMQISATLVK-GKARVQFGANKSQYSLTRAQ 399
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Best Local Similarity 22.9%; Pred. No. 0.01
Matches 49; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
   PF-0093 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0093 US
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,765
FILING DATE: FILE HEREWITH
ATTORNEY/AGENT INFORMATION:
                 TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
REFERENCE/DOCKET NUMBER:
                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acids
                                                                                                                                                single
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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ADDRESSEE: Incyte Ph
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CLONE: 1064914
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TOPOLOGY: lin
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STATE:
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189 DEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNORQDYLNGAVSG 248
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                                                                                                                                                                                      9 DDSPSTSGGSSDGDQRESVQQEPER--------EQVQPKKKECKISSKTAA 51
                                                                                                                                                                                                                                                                                               : : |: ||| :|
52 KLSTSAKRIQKELAEITLDPP---PNCSAGPKGDNIYEWRSTIL--GPPGSVY------99
                                                                      90; Indels 36;
5.3%; Score 119; DB 2; Length 201; 21.1%; Pred. No. 0.018; tive 42; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09196525
Patent No. 598983
GENERAL INFORMATION:
APPLICANT: ALTURON, Janice
APPLICANT: GOli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBLOUITIN-CONJUGATING
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 SVIMQISATLV-KGKARVQFGANKSQYSLTRAQ 399
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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189 DEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSG 248
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                                                                                                                                                                                                                                                                 -----EQVQPKKKEGKISSKTAA 51
                                                                                                                                                                                                                                          249 SVQ-ATDRIMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILK
                                                                                                                       Gaps
                                                                                                                         36;
                                                                               Length 201;
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN UBIQUITIN-CONJUGATING
TITLE OF INVENTION: ENZYME
                                                                             Ouery Match 5.3%; Score 119; DB 2; Lø
Best Local Similarity 21.1%; Pred. No. 0.018;
Matches 45; Conservative 42; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                       368 SVIMQISATLV-KGKARVQFGANKSQYSLTRAQ 399
                                                                                                                                                                                                                                                                                                                                                                                                                                      155 KVLLSICSLLTDXNPADPLVGSIATOYMTNRAE 187
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0093 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FRASED VERSION 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,317
                                                                                                                                                                                                    9 DDSPSTSGGSSDGDQRESVQQEPER--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09318317
Patent No. 6172199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE; Diskett.
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; LIBRARY: PGANNOT01
; CLONE: 61887
US-09-196-525-1
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JS-09-318-317-1
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                                                                                                                    9 DDSPSTSGGSSDGDQRESVQQEPER-------EQVQPKKKEGKISSKTAA 51
                                                                                    189 DEDEEMPEDTEDLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNORODYLNGAVSG
                                                                                                                                                                                            52 KISTSAKRIQKELARITLDPP---PNCSAGPKGDNIYEWRSTIL--GPPGSVY----
                                             Gaps
                                           36;
Ouery Match 5.3%; Score 119; DB 3; Length 201; Best Local Similarity 21.1%; Pred. No. 0.018; Matches 45; Conservative 42; Mismatches 90; Indels
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